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(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES (57) Abstract <p>The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.</p>		

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5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer
5 tremendous promise for the understanding, diagnosis, and treatment of human diseases. In
addition, probes capable of specifically hybridizing to loci distributed throughout the human
genome find applications in the construction of high resolution chromosome maps and in the
identification of individuals.

In the past, the characterization of even a single human gene was a painstaking
10 process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA
sequencing, and computer technology have merged to greatly accelerate the rate at which
human genes can be isolated, sequenced, mapped, and characterized. Cloning vectors such as
yeast artificial chromosomes (YACs) and bacterial artificial chromosomes (BACs) are able to
accept DNA inserts ranging from 300 to 1000 kilobases (kb) or 100-400 kb in length
15 respectively, thereby facilitating the manipulation and ordering of DNA sequences distributed
over great distances on the human chromosomes. Automated DNA sequencing machines
permit the rapid sequencing of human genes. Bioinformatics software enables the
comparison of nucleic acid and protein sequences, thereby assisting in the characterization of
human gene products.

20 Currently, two different approaches are being pursued for identifying and
characterizing the genes distributed along the human genome. In one approach, large
fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading
frames in these genomic sequences are identified using bioinformatics software. However,
this approach entails sequencing large stretches of human DNA which do not encode proteins
25 in order to find the protein encoding sequences scattered throughout the genome. In addition
to requiring extensive sequencing, the bioinformatics software may mischaracterize the
genomic sequences obtained. Thus, the software may produce false positives in which non-
coding DNA is mischaracterized as coding DNA or false negatives in which coding DNA is
misabeled as non-coding DNA.

30 An alternative approach takes a more direct route to identifying and characterizing
human genes. In this approach, complementary DNAs (cDNAs) are synthesized from

isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended
5 cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene
10 from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the
15 mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs. (Adams *et al.*, *Nature* 377:3-174, 1996; Hillier *et al.*, *Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been
20 obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences
25 derived from the 5' ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding genes, those genes encoding proteins which are
30 secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often

involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells.

In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon- α , interferon- β , interferon- γ , and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. In addition, portions of signal sequences may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches

have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, *et al.*, *Nature Genetics* 6: 236-244, 1994). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al.*, *Genome Res.* 6:327-335, 1996). Both of these approaches
5 have their limits due to a lack of specificity or of comprehensiveness.

The present 5' ESTs may be used to efficiently identify and isolate upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. (Theil, *BioFactors* 4:87-93, 1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or
10 protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of secretory protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding
15 sequences of genes encoding secretory proteins.

Summary of the Invention

The present invention relates to purified, isolated, or recombinant ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. The term
20 "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. These sequences will be referred to hereinafter as "5' ESTs." As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these
25 clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus,
30 creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4 - 10^6 fold purification of the native message.

Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5' EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5' ESTs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched 5' ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5' ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Stringent", moderate, and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary.

Thus, 5' ESTs in cDNA libraries in which one or more 5' ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant 5' ESTs" as defined herein. Likewise, 5' ESTs in a population of plasmids in which one or more 5' EST of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are "enriched recombinant 5' ESTs" as defined herein. However, 5' ESTs in cDNA libraries in which 5' ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in

which backbone molecules having a 5' EST insert are extremely rare, are not "enriched recombinant 5' ESTs."

In particular, the present invention relates to 5' ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Such 5' ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5' ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5' ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5' ends of the coding sequences of the mRNAs from which the 5' ESTs are derived. These cDNAs will be referred to hereinafter as "full length cDNAs." These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full length cDNA sequences may be used to express the proteins corresponding to the 5' ESTs. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or

controlling a variety of human conditions. The 5' ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5' EST was derived.

Alternatively, the 5' ESTs may be used to obtain and express extended cDNAs
5 encoding portions of the secreted protein. The portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off. The portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. Alternatively, the portions may
10 comprise at least 15 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In some embodiments, the portions may comprise at least 25 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs or full length cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the
15 extended cDNAs, full length cDNAs, or fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the
20 signal peptides encoded by the extended cDNAs or full length cDNAs may also be obtained.

In some embodiments, the extended cDNAs obtained using the 5' ESTs include the signal sequence. In other embodiments, the extended cDNAs obtained using the 5' ESTs may include the full coding sequence for the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs obtained using the 5'
25 ESTs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression.

As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the extended cDNAs or full length cDNAs obtained using the 5'
30 ESTs may be useful in treating or controlling a variety of human conditions.

The 5' ESTs (or cDNAs or genomic DNAs obtained therefrom) may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the 5' ESTs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the 5' ESTs, such as promoters or upstream regulatory sequences.

Finally, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the 5' ESTs of the present invention (SEQ ID NOs: 38-305 are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under the designations listed next to the SEQ ID NOs in II). The inserts may be recovered from the deposited materials by growing the appropriate clones on a suitable medium. The Bluescript DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One aspect of the present invention is a purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-305 or having a sequence complementary thereto. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.

Yet another aspect of the present invention is a purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-305 or one of the sequences complementary thereto. In one embodiment, the nucleic acid is recombinant.

A further aspect of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-305.

Still another aspect of the present invention is a method of making a cDNA encoding a human secretory protein, said human secretory protein being partially encoded by one of SEQ ID NOs 38-305, comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence complementary to one of SEQ ID NOs: 38-305; hybridizing said primer to an mRNA in said collection that encodes said protein; reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA; making a second cDNA strand complementary to said first cDNA strand; and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another aspect of the invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the

cDNA comprises the full protein coding sequence of said protein which sequence is partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-305, comprising the steps of obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-305; contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-305 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA; identifying a cDNA which hybridizes to said detectable probe; and isolating said cDNA which hybridizes to said probe.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a cDNA comprising one of the sequence of SEQ ID NOs: 38-305, comprising the steps of contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA; hybridizing said first primer to said polyA tail; reverse transcribing said mRNA to make a first cDNA strand; making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-305; and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

In one embodiment of the method described in the two paragraphs above, the second cDNA strand is made by contacting said first cDNA strand with a first pair of primers, said

first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-305 and a third primer having a sequence therein which is included within the sequence of said first primer; performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product; contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NOs: 38-305, and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is the method described four paragraphs above in which the second cDNA strand is made by contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-305; hybridizing said second primer to said first strand cDNA; and extending said hybridized second primer to generate said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-305 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a protein comprising one of the sequences of SEQ ID NOs: 306-573, comprising the steps of obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NOs: 38-305; inserting said cDNA in an expression vector such that said cDNA is

operably linked to a promoter; introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and isolating said protein.

Another aspect of the present invention is an isolated protein obtainable by the method described in the preceding paragraph.

5 Another aspect of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining DNAs located upstream of the nucleic acids of SEQ ID NOs: 38-305 or the sequences complementary thereto; screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and isolating said DNA comprising said identified promoter. In one embodiment, the obtaining step comprises
10 chromosome walking from said nucleic acids of SEQ ID NOs: 38-305 or sequences complementary thereto. In another embodiment, the screening step comprises inserting said upstream sequences into a promoter reporter vector. In another embodiment, the screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

15 Another aspect of the present invention is an isolated promoter obtainable by the method described above.

Another aspect of the present invention is an isolated or purified protein comprising one of the sequences of SEQ ID NOs: 306-573.

Another aspect of the present invention is the inclusion of at least one of the
20 sequences of SEQ ID NOs: 38-305, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305, or a fragment thereof of at least 15 consecutive nucleotides in an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length. In one embodiment, the array includes at least two of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of
25 at least 15 consecutive nucleotides. In another embodiment, the array includes at least five of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

Another aspect of the present invention is a promoter having a sequence selected from the group consisting of SEQ ID NOs: 31, 34, and 37.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they derived.

Figure 2 shows the distribution of Von Heijne scores for 5' ESTs in each of the categories described herein and the probability that these 5' ESTs encode a signal peptide.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5' ESTs.

Figure 4 (description of promoters structure isolated from SignalTag 5' ESTs) provides a schematic description of promoters isolated and the way they are assembled with the corresponding 5' tags.

Detailed Description of the Preferred Embodiment

Table IV is an analysis of the 43 amino acids located at the N terminus of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Table V shows the distribution of 5' ESTs in each category described herein and the number of 5' ESTs in each category having a given minimum Von Heijne's score.

Table VI shows the distribution of 5' ESTs in each category described herein with respect to the tissue from which the 5' ESTs of the corresponding mRNA were obtained.

Table VII describes the transcription factor binding sites present in each of these promoters.

I. General Methods for Obtaining 5' ESTs derived from mRNAs with intact 5' ends

In order to obtain the 5' ESTs of the present invention, mRNAs with intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs with intact 5' ends as described below: either chemical (1) or enzymatic (2).

1. Chemical Methods for Obtaining mRNAs having Intact 5' Ends

One of these approaches is a chemical modification method involving derivatization of the 5' ends of the mRNAs and selection of the derivatized mRNAs. The 5' ends of eukaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine

methyated at the 7 position. The cap is joined to the first transcribed base of the mRNA by a 5', 5'-triphosphate bond. In some instances, the 5' guanosine is methyated in both the 2 and 7 positions. Rarely, the 5' guanosine is trimethyated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5' ends, the 5' cap is specifically
5 derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methyated guanosine at the 5' end of the mRNA and the ribose linked to the base at the 3' terminus of the mRNA, possess 2', 3'-cis diols.

Optionally, the 2', 3'-cis diol of the 3' terminal ribose may be chemically
10 modified, substituted, converted, or eliminated, leaving only the ribose linked to the methyated guanosine at the 5' end of the mRNA with a 2', 3'-cis diol. A variety of techniques are available for eliminating the 2', 3'-cis diol on the 3' terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3' terminal ribose is a 3'-phosphate, 2'-phosphate or (2', 3')-cyclophosphate.
15 Thereafter, the fragment which includes the original 3' ribose may be eliminated from the mixture through chromatography on an oligodT column. Alternatively, a base which lacks the 2', 3'-cis diol may be added to the 3' end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of a nucleoside diphosphate to the 3' end of messenger RNA.

20

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of mRNA

One μg of RNA was incubated in a final reaction medium of 10 μl in the presence of 5 U of T₄ phage RNA ligase in the buffer provided by the manufacturer (Gibco -
25 BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 μl of ³²pCp (Amersham #PB 10208). The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2', 3'-cis diol at the 3' ribose, the 2', 3'-cis diol present at the 5' end of the mRNA may be oxidized using reagents such as NaBH₄,
30 NaBH₃CN, or sodium periodate, thereby converting the 2', 3'-cis diol to a dialdehyde.

Example 2 describes the oxidation of the 2', 3'-cis diol at the 5' end of the mRNA with sodium periodate.

EXAMPLE 2

5 Oxidation of 2', 3'-cis diol at the 5' End of the mRNA with Sodium Periodate

0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by *in vitro* transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the *in vitro* transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, m7G(5')ppp(5')G. This compound, recognized by the polymerase, was incorporated into the 5' end of the nascent transcript during the initiation of transcription but was not incorporated during the extension step. Consequently, the resulting RNA contained a cap at its 5' end. The sequences of the oligoribonucleotides produced by the *in vitro* transcription reaction were:

+Cap:

5'm7GpppGCAUCCUACUCCCAUCCAAUCCACCCUAACUCCUCCCAUCUCCAC-
3' (SEQ ID NO:1)

20 -Cap:

5'-pppGCAUCCUACUCCCAUCCAAUCCACCCUAACUCCUCCCAUCUCCAC-3'
(SEQ ID NO:2)

The oligoribonucleotides were dissolved in 9 µl of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 µl of freshly prepared 0.1 M sodium periodate solution. The mixture was incubated for 1 hour in the dark at 4°C or room temperature. Thereafter, the reaction was stopped by adding 4 µl of 10% ethylene glycol. The product was ethanol precipitated, resuspended in at least 10 µl of water or appropriate buffer and dialyzed against water.

The resulting aldehyde groups may then be coupled to molecules having a reactive amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5' ends of the mRNAs. Molecules having reactive amine groups

which are suitable for use in selecting mRNAs having intact 5' ends include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

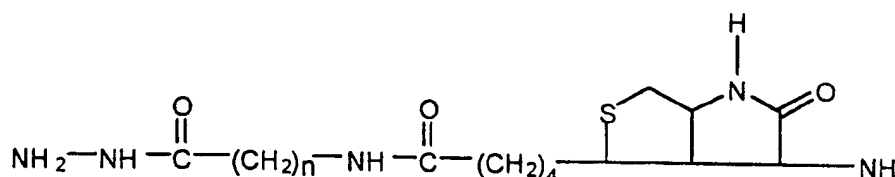
5

EXAMPLE 3

Coupling of the Dialdehyde at the 5' End of Transcripts with Biotin

The oxidation product obtained in Example 2 was dissolved in 50 μ l of sodium acetate at a pH between 5 and 5.2 and 50 μ l of freshly prepared 0.02 M solution of biotin hydrazide in a methoxyethanol/water mixture (1:1) of formula:

10



In the compound used in these experiments, $n=5$. However, it will be appreciated that other commercially available hydrazides may also be used, such as molecules of the above formula in which n varies from 0 to 5. The mixture was then incubated for 2 hours at 37°C, precipitated with ethanol and dialyzed against distilled water. Example 4 demonstrates the specificity of the biotinylation reaction.

15

EXAMPLE 4

20

Specificity of Biotinylation of Capped Transcripts

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

Sample 1. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2 and labeled with 32 pCp as described in Example 1.

25

Sample 2. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2, labeled with 32 pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Sample 3. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2 and labeled with ^{32}pCp as described in Example 1.

Sample 4. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2, labeled with ^{32}pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Samples 1 and 2 had identical migration rates, demonstrating that the uncapped RNAs were not oxidized and biotinylated. Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration. The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

10

In some cases, mRNAs having intact 5' ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

20

The mRNAs having intact 5' ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5' ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the biotinylated mRNAs from the beads following enrichment.

25

EXAMPLE 5

Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

30

The streptavidin coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a

hybridization buffer (1.5 M NaCl, pH 5 - 6). After incubating for 30 minutes, the unbound and nonbiotinylated material was removed. The beads were then washed several times in water with 1% SDS. The beads thus obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

5 Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6

Efficiency of Recovery of Biotinylated mRNAs

10 The efficiency of the recovery procedure was evaluated as follows. Capped RNAs were labeled with ^{32}pCp , oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

15 The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

 Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

20 In an alternative method for obtaining mRNAs having intact 5' ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3' end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3' end of the mRNA. For example, pCp may be attached to the 3' end of the mRNA using T4 RNA ligase as described in example 1. However, as discussed above, blocking the 3' end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described in Example 7.

EXAMPLE 7Derivatization of Oligonucleotides

An oligonucleotide phosphorylated at its 3' end was converted to a 3' hydrazide in 3' by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula
5 $H_2N(R1)NH_2$ at about 1 to 3 M, and at pH 4.5 at a temperature of 8°C overnight. This incubation was performed in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M.

The derivatized oligonucleotide was then separated from the other agents and products using a standard technique for isolating oligonucleotides.

10 As discussed above, the mRNAs to be enriched may be treated to eliminate the 3' OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3' OH, such as pCp, as described in Example 1. Alternatively, the 3' OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

15

EXAMPLE 8Elimination of 3' OH Groups of mRNA Using Alkaline Hydrolysis

In a total volume of 100 µl of 0.1 N sodium hydroxide, 1.5 µg mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol.

20 Following the optional elimination of the 3' OH groups, the diol groups at the 5' ends of the mRNAs are oxidized as described below in Example 9.

EXAMPLE 9Oxidation of Diols of mRNA

25 Up to 1 OD unit of RNA was dissolved in 9 µl of buffer (0.1 M sodium acetate, pH 6-7) or water and 3 µl of freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 µl of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was
30 resuspended in at least 10 µl of water or appropriate buffer and dialyzed against water.

Following oxidation of the diol groups at the 5' ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

EXAMPLE 10

5 Ligature of Aldehydes of mRNA to Derivatized Oligonucleotides

The oxidized mRNA was dissolved in an acidic medium such as 50 µl of sodium acetate pH 4-6. Fifty µl of a solution of the derivatized oligonucleotide were added in order to obtain an mRNA:derivatized oligonucleotide ratio of 1:20. The mixture was reduced with a borohydride and incubated for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was
10 then ethanol precipitated, resuspended in 10 µl or more of water or appropriate buffer and dialyzed against distilled water. If desired, the resulting product may be analyzed using acrylamide gel electrophoresis, HPLC analysis, or other conventional techniques.

Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse
15 transcription reaction may be performed as described in Example 11 below.

EXAMPLE 11

Reverse Transcription of mRNAs Ligatured to Derivatized Oligonucleotides

An oligodeoxyribonucleotide was derivatized as follows. Three OD units of an
20 oligodeoxyribonucleotide of sequence 5'ATCAAGAATTCGCACGAGACCATTAA3' (SEQ ID NO:3) having 5'-OH and 3'-P ends were dissolved in 70 µl of a 1.5 M hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25) containing 2 µg of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was incubated for 2 h 30 min at 22°C and then precipitated twice in LiClO₄/acetone. The pellet
25 was resuspended in 200 µl of 0.25 M hydrazine and incubated at 8°C from 3 to 14 h. Following the hydrazine reaction, the mixture was precipitated twice in LiClO₄/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of placenta having sides of 2 cm which had been stored at -80°C. The total RNA was extracted using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify
30 the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μ g of the placental mRNAs were oxidized as described above in Example 9. The derivatized oligonucleotide was joined to the mRNAs as described in Example 10 above except that the precipitation step was replaced by an exclusion chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined to mRNAs. Exclusion chromatography was performed as follows:

Ten ml of Ultrogel AcA34 (BioSeptra#230151) gel, a mix of agarose and acrylamide, were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

Ten μ l of the mRNA which had reacted with the derivatized oligonucleotide were mixed in 39 μ l of 10 mM urea and 2 μ l of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a 0.45 μ m diameter filter.

The column was then loaded with the mRNAs coupled to the oligonucleotide. As soon as the sample had penetrated, equilibration buffer was added. Hundred μ l fractions were then collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Thus, fractions 3 to 15 were combined and precipitated with ethanol.

To determine whether the derivatized oligonucleotide was actually linked to mRNA, one tenth of the combined fractions were spotted twice on a nylon membrane and hybridized to a radioactive probe using conventional techniques. The 32 P labeled probe used in these hybridizations was an oligodeoxyribonucleotide of sequence 5'TAATGGTCTCGTGCGAATTCTTGAT3' (SEQ ID NO:4) anticomplementary to the derivatized oligonucleotide. A signal observed after autoradiography, indicated that the derivatized oligonucleotide had been truly joined to the mRNA.

The remaining nine tenth of the mRNAs which had reacted with the derivatized oligonucleotide was reverse transcribed as follows. A reverse transcription reaction was

carried out with reverse transcriptase following the manufacturer's instructions and 50 pmol of nonamers with random sequence as primers.

To ensure that reverse transcription had been carried out through the cap structure, two types of experiments were performed.

5 In the first approach, after elimination of RNA of the cDNA:RNA heteroduplexes obtained from the reverse transcription reaction by an alkaline hydrolysis, a portion of the resulting single stranded cDNAs was spotted on a positively charged membrane and hybridized, using conventional methods, to a ³²P labeled probe having a sequence identical to that of the derivatized oligonucleotide. Control spots containing, 1 pmol, 100 fmol, 50 fmol,
10 10 fmol and 1 fmol of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide were included. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed. These results demonstrate that the reverse transcription can be performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-
15 5' bond of the cap of eukaryotic messenger RNAs.

In the second type of experiment, the single stranded cDNAs obtained from the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for alpha globin, dehydrogenase, pp15 and elongation factor E4 were carried out using the following pairs of
20 oligodeoxyribonucleotide primers.

alpha-globin

GLO-S: 5'CCG ACA AGA CCA ACG TCA AGG CCG C3' (SEQ ID NO:5)

GLO-As: 5'TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

25

dehydrogenase

3 DH-S: 5'AGT GAT TCC TGC TAC TTT GGA TGG C3' (SEQ ID NO:7)

3 DH-As: 5'GCT TGG TCT TGT TCT GGA GTT TAG A3' (SEQ ID NO:8)

30

pp15

PP15-S: 5'TCC AGA ATG GGA GAC AAG CCA ATT T3' (SEQ ID NO:9)

PP15-As: 5' AGG GAG GAG GAA ACA GCG TGA GTC C3' (SEQ ID NO:10)

Elongation factor E4

EFA1-S: 5' ATG GGA AAG GAA AAG ACT CAT ATC A3' (SEQ ID NO:11)

5 EF1A-As: 5' AGC AGC AAC AAT CAG GAC AGC ACA G3' (SEQ ID NO:12)

Second, non specific amplifications were also carried out with the antisense oligodeoxyribonucleotides of the pairs described above and with a primer derived from the sequence of the derivatized oligodeoxyribonucleotide
10 (5' ATCAAGAATTCGCACGAGACCATT A3') (SEQ ID NO:13).

One twentieth of the following RT-PCR product samples were run on a 1.5% agarose gel and stained with ethidium bromide.

Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

15 Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

20 Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

25 Sample 7: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

Sample 8: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

30 A band of the size expected for the PCR product was observed only in samples 1, 3, 5 and 7, thus indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized oligonucleotide. The presence of PCR products of the expected size in the samples equivalent to above samples 1 and 3 indicated that the
5 derivatized oligonucleotide had been linked to mRNA.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5' ends as illustrated in Figure 1. Further detail regarding the chemical approaches for obtaining such mRNAs are disclosed in International Application No.
10 WO96/34981, published November 7, 1996, which is incorporated herein by reference. Strategies based on the above chemical modifications to the 5' cap structure may be utilized to generate cDNAs selected to include the 5' ends of the mRNAs from which they derived. In one version of such procedures, the 5' ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer
15 complementary to the 5' end of the mRNA. Single stranded RNAs are eliminated to obtain a population of cDNA/mRNA heteroduplexes in which the mRNA includes an intact 5' end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5' end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first
20 cDNA strands which include the 5' end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci. *et al.*, *Genomics* 37:327-336, 1996, the disclosures of which are incorporated herein by reference, may be employed to select cDNAs which include the sequence derived from the 5' end of the coding sequence of the mRNA.

25 Following ligation of the oligonucleotide tag to the 5' cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a primer complementary to the oligonucleotide tag.

2. Enzymatic Methods for Obtaining mRNAs having Intact 5' Ends

Other techniques for selecting cDNAs extending to the 5' end of the mRNA from which they are derived are fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc
5 complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al.*, *Gene* **150**:243-250, 1994, the disclosures of which are incorporated herein by reference.

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate groups present on the 5' ends of uncapped incomplete mRNAs.
10 Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase. An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3' end, is then ligated to the phosphate present at the 5' end of the decapped mRNA using T4 RNA ligase. The oligonucleotide may include a
15 restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

EXAMPLE 12

Enzymatic Approach for Obtaining 5' ESTs

20 Twenty micrograms of PolyA+ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA was hydrolysed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi *et al.*, *Biochemistry* **15**: 2185-2190, 1976) and a hemi 5'DNA/RNA-3' oligonucleotide having an unphosphorylated 5' end, a stretch of adenosine ribophosphate at the 3' end, and an EcoRI
25 site near the 5' end was ligated to the 5'P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this procedure are preferably 30 to 50 bases in length. Oligonucleotides having an unphosphorylated 5' end may be synthesized by adding a fluorochrome at the 5' end. The inclusion of a stretch of adenosine ribophosphates at the 3' end of the oligonucleotide increases ligation efficiency. It will be appreciated that the
30 oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5' end of the decapped mRNA, first and second strand cDNA synthesis is carried out using conventional methods or those specified in EP0 625,572 and Kato *et al. supra*, and Dumas Milne Edwards, *supra*, the disclosures of which are incorporated herein by reference. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato *et al. supra* or other nucleic acid vectors known to those skilled in the art using techniques such as those described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference.

II. Obtention and Characterization of the 5' ESTs of the Present Invention

The 5' ESTs of the present invention were obtained using the aforementioned chemical and enzymatic approaches for enriching mRNAs for those having intact 5' ends as described below.

1. Obtention of 5' ESTS Using mRNAs with Intact 5' Ends

First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA With Intact 5' Ends

Total human RNAs or polyA⁺ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as follows. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczynski and Sacchi, *Analytical Biochemistry* **162**:156-159, 1987). PolyA⁺ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* **69**:1408-1412, 1972 in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA⁺ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the polyA⁺ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with

less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

5 Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for enriching mRNAs for those having intact 5' ends were employed to obtain 5' ESTs from various tissues. In both approaches, an oligonucleotide tag was attached to the 5' ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures. To facilitate the processing of single stranded and double
10 stranded cDNA obtained in the construction of the libraries, the same nucleotidic sequence was used to design the ligated oligonucleotide in both chemical and enzymatic approaches. Nevertheless, in the chemical procedure, the tag used was an oligodeoxyribonucleotide which was linked to the cap of the mRNA whereas in the enzymatic ligation, the tag was a chimeric hemi 5'DNA/RNA3' oligonucleotide which was ligated to the 5' end of decapped mRNA as
15 described in example 12.

Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200 to 500 ng of mRNA using a probe complementary to the oligonucleotide tag before performing the first strand synthesis as described in example 14.

20

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed using the Superscript II (Gibco BRL) or
25 the Rnase H Minus M-MLV (Promega) reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

30 For both the chemical and the enzymatic methods, the second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5' end of the

ligated oligonucleotide described in Example 12. Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in
5 Example 15 below.

EXAMPLE 15

Cloning of cDNAs derived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA
10 polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (Aca, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned
15 into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were then selected as described in
Example 16 below.

20

EXAMPLE 16

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows.
25 Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was
30 hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25

bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocols such as the one described in the Gene Trapper kit available from Gibco BRL may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated to typically rank between 90 and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 17

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

2. Computer analysis of the Obtained 5' ESTs: Construction of NetGene and SignalTag databases

The sequence data from the 44 cDNA libraries made as described above were transferred to a proprietary database, where quality control and validation steps were performed. A proprietary base-caller, working using a Unix system, automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The proprietary base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5' ESTs were entered in NetGene™, a proprietary database called for storage and manipulation as described below. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media include magnetically, optically, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a diversity of formats. For instance, the sequence data may be stored as text in a word processing file, such as Microsoft WORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data. Once the sequence data has been stored, it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other

known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL), BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul *et al*, *J. Mol. Biol.* 215: 403, 1990) and FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85: 2444, 1988). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

Motifs which may be detected using the above programs and those described in Example 28 include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NetGene™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

Elimination of Undesired Sequences from Further Consideration

5' ESTs in the NetGene™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table I.

To eliminate 5' ESTs encoding tRNAs from further consideration, the 5' EST sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5' ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80%
5 homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to the sequences of the two known mitochondrial genomes for
10 which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were
15 identified as mtRNAs and eliminated from further consideration.

Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S=144. All sequences having more than 90% homology over at least 40 nucleotides were identified as exogenous
20 contaminants. Of the 42 cDNA libraries examined, the average percentages of prokaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be identified as a sequence specific to fungi. The others were either fungal or prokaryotic sequences having homologies with vertebrate sequences or including repeat sequences which had not been masked during the electronic comparison.

25 In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of the sequences in the libraries contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1
30 repeats and the remaining 1.2% were derived from the other screened types of repetitive sequences. These percentages are consistent with those found in cDNA libraries prepared by

other groups. For example, the cDNA libraries of Adams *et al.* contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA library (Adams *et al.*, *Nature* 377:174, 1996).

- 5 The sequences of those 5' ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

EXAMPLE 19

10 Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5' ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database. The 6655 5' ESTs which matched a known human mRNA were then
15 realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

- 20 This analysis revealed that the sequences incorporated in the NetGene™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5' ends of their corresponding mRNAs, the following analysis was
25 performed.

EXAMPLE 20

Determination of Efficiency of 5' EST Selection

- To determine the efficiency at which the above selection procedures isolated 5' ESTs
30 which included sequences close to the 5' end of the mRNAs from which they derived, the sequences of the ends of the 5' ESTs derived from the elongation factor 1 subunit α and

ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5' ESTs which included the authentic transcription start sites.

5 For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the NetGene™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for
10 comparison. The 5' ends of more than 85% of 5' ESTs derived from mRNAs included in the GeneBank database were located close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends
15 of their corresponding mRNAs.

The EST libraries made above included multiple 5' ESTs derived from the same mRNA. The sequences of such 5' ESTs were compared to one another and the longest 5' ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous
20 sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5' ESTs and Calculation of Novelty Indices for cDNA Libraries

25 For each sequenced EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S=107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5' end were grouped. The longest sequence found in the cluster was used as representative of the group. A global
30 clustering between libraries was then performed leading to the definition of super-contigs.

To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: $NR = 100 \times (\text{Number of new unique sequences found in the library} / \text{Total number of sequences from the library})$. Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5' ESTs in NetGene™ was screened to identify those 5' ESTs bearing potential signal sequences as described in Example 22 below.

EXAMPLE 22

Identification of Potential Signal Sequences in 5' ESTs

The 5' ESTs in the NetGene™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG codon and extending to the end of the EST. Approximately half of the cDNA sequences in NetGene™ contained such an ORF. The ORFs of these 5' ESTs were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res.* 14:4683-4690, 1986, the disclosure of which is incorporated herein by reference. Those 5' EST sequences encoding a stretch of at least 15 amino acid long with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5' ESTs which matched a known human mRNA or EST sequence and had a 5' end more than 20 nucleotides downstream of the known 5' end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SignalTag™.

To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figure 2 and table IV.

Using the above method of identification of secretory proteins, 5' ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637, the disclosure of which is incorporated herein by reference. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST signal sequence confirms that the 5' EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1⁺ (as described below in example 30), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5' ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences as described in Example 24 below.

EXAMPLE 24

Categorization of 5' ESTs Encoding a Signal Peptide

Those 5' ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SignalTagTM database, 947 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5' direction. Of the sequences in the SignalTagTM database, 150 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5' direction were designated "EST." Of the sequences in the SignalTagTM database, 599 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5' direction were designated "VERT-ext." Of the sequences in the SignalTagTM database, 23 of the 5' ESTs having a Von Heijne's score of at

least 3.5 fell into this category. Included in this category was a 5' EST which extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction. A 5' EST which extended the sequence of a human tumor suppressor gene in the 5' direction was also identified.

5 Table V shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

3. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5' ESTs or Extended cDNAs

10

Each of the 5' ESTs was also categorized based on the tissue from which its corresponding mRNA was obtained, as described below in Example 25.

EXAMPLE 25

15

Categorization of Expression Patterns

Table VI shows the distribution of 5' ESTs in each of the above defined category with respect to the tissue from which the 5' ESTs of the corresponding mRNA were obtained.

20 Table II provides the sequence identification numbers of 5' EST sequences derived from muscle and other mesodermal tissues, the categories in which these sequences fall, and the von Heijne's score of the signal peptides which they encode. The 5' EST sequences and the amino acid sequences they encode are provided in the appended sequence listings. Table III provides the sequence ID numbers of the 5' ESTs and the sequences of the signal peptides which they encode. The sequences of the 5' ESTs and the polypeptides they encode are provided in the sequence listing appended hereto.

25

The sequences of DNA SEQ ID NOs: 38-305 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or ambiguities on both strands. Such fragments may be obtained from the plasmids stored in the inventors' laboratory or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers
30 which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or

error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity.

In addition to categorizing the 5' ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of expression, over expression, or under expression of an mRNA corresponding to a 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy individuals with those from individuals suffering from a particular disease, 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the ESTs themselves.

EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to 5' ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5' ESTs or extended cDNAs (obtainable as described below in example 27) may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277, the entire contents of which are hereby incorporated by reference. Briefly, a 5' EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3,

T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5' EST or extended cDNA has 100 or more nucleotides. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (*i.e.* biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (*i.e.* RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The 5' ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A, the entire contents of which are incorporated by reference. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so-called tagging endonuclease is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so-called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2

to 200 ditags. The tag sequences are then determined and compared to the sequences of the 5' ESTs or extended cDNAs to determine which 5' ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs or extended cDNAs in the cell,
5 tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (*i.e.* extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon),
10 extended cDNAs, 5' ESTs or fragments thereof of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length. More preferably, the fragments are at least 100 nucleotide long. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments, the fragments may be more than 500 nucleotide long.

15 For example, quantitative analysis of gene expression may be performed with full length cDNAs as defined below, extended cDNAs, 5' ESTs, or fragments thereof in a complementary DNA microarray as described by Schena *et al.* (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). Full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter
20 plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

25 Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm² microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a
30 fluorescence laser scanning device fitted with a custom filter set. Accurate differential

expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in complementary DNA arrays as described by Pietu *et al.* (*Genome Research* 6:492-503, 1996). The full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5' ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology* 14: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5' ESTs or extended cDNAs are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al.*, *supra* and application of different electric fields (Sonowsky *et al.*, *supra.*), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

III. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs using 5' ESTs. Example 28 below provides experimental results, using the method explained in example 27, describing several extended cDNAs including the entire coding sequence and authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5' ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 38-305. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 38-305. In further embodiments, the extended cDNAs encode at least 30 amino amino acids of the sequences of SEQ ID NOs: 38-305. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 38-305.

EXAMPLE 27

General Method for Using 5' ESTs to Clone and Sequence cDNAs which Include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA

The following general method has been used to quickly and efficiently isolate extended cDNAs having the authentic 5' ends of their corresponding mRNAs as well as

the full protein coding sequence and including sequence adjacent to the sequences of the 5' ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST in the NetGene™ database, including those 5' ESTs encoding polypeptides belonging to secreted proteins. The method is summarized in figure 3.

5

1. Obtention of Extended cDNAs

a) First strand synthesis

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a
10 49 nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. For example, the primer may have the following sequence: 5'-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG TAC TGG TTT TTT TTT TTT TTVN -3' (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT
15 sequence and used to prime the first strand synthesis. Using this primer and a reverse transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3' polyA site of the RNAs is generated.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer are
20 eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST and the known 3' end added by the poly dT primer used in the first strand
25 synthesis. Softwares used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais *et al.*, *Nucleic Acids Res.* 19: 3887-3891, 1991) such as PC-Rare (<http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html>).

Preferably, the nested primers at the 5' end are separated from one another by four to nine bases. The 5' primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

Preferably, the nested primers at the 3' end are separated from one another by four to nine bases. For example, the nested 3' primers may have the following sequences: (5'- CCA GCA GAG TCA CGA GAG AGA CTA CAC GG -3'(SEQ ID NO:15), and 5'- CAC GAG AGA GAC TAC ACG GTA CTG G -3' (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

2. Sequencing of Full Length Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described in the following section.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.* the polyA tract and sometimes the polyadenylation signal, as illustrated in figure 3. Such full length extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et al.*, *Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined. When Northern blot data are available, the size of the mRNA detected for a given PCR

product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in
5 example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector
10 pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended
15 cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is
20 determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3' end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case
25 b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the
30 aforementioned procedure. In this case, contiguation of long fragments is then performed on walking sequences that have already contiguated for uncloned PCR products during

primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

5 4. Computer analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below. Before searching the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest (vector RNAs, transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs) are discarded using methods essentially similar to those described for 5'ESTs in Example 18.

10 *a) Identification of structural features*

Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

15 A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 100 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. Stretches having more than 90% homology over 8 nucleotides are identified as polyA tails using BLAST2N.

20 To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are first searched for the canonic polyadenylation AAUAAA signal and, if the canonic signal is not detected, for the alternative AUUAAA signal (Sheets *et al.*, *Nuc. Acids Res.* 18: 5799-5805, 1990). If neither of these consensus polyadenylation signals is found, the canonic motif is searched again allowing one mismatch to account for possible sequencing errors. More than 85 %
25 of identified polyadenylation signals of either type actually ends 10 to 30 bp from the polyA tail. Alternative AUUAAA signals represents approximately 15 % of the total number of identified polyadenylation signals.

b) Identification of functional features

30 Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (*Nuc. Acids Res.* 14: 4683-4690, 1986), the disclosure of which is incorporated herein by reference as described in Example 22.

c) Homology to either nucleotidic or proteic sequences

Categorization of full-length sequences may be achieved using procedures essentially similar to those described for 5'ESTs in Example 24.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences (*i.e.* the sequences encoding the signal peptide and the mature protein remaining after the signal peptide is cleaved off) may be obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only the coding sequences for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides.

Similarly, nucleic acids containing any other desired portion of the coding sequences for the secreted protein may be obtained. For example, the nucleic acid may contain at least 10 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 15 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. Alternatively, the nucleic acid may contain at least 20 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 25 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In yet another embodiment, the nucleic acid may contain at least 40 consecutive bases of an extended cDNA such as one of the extended cDNAs described below.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants
5 or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

The extended cDNAs derived from the 5' ESTS of the present invention were
10 obtained as described in Example 28 below.

EXAMPLE 28

Characterization of cloned extended cDNAs obtained using 5' ESTs

The procedure described in Example 27 above was used to obtain the extended
15 cDNAs derived from the 5' ESTs of the present invention in a variety of tissues. The following list provides a few examples of thus obtained extended cDNAs.

Using this approach, the full length cDNA of SEQ ID NO:17 (internal identification number 48-19-3-G1-FL1) was obtained. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MKKVLLLITAILAVAVG (SEQ ID NO:
20 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:19 (internal identification number 58-34-2-E7-FL2) was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVIWTS (SEQ ID NO:20) having a von Heijne score of 5.5.

25 Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21 (internal identification number 51-27-1-E8-FL1). This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLP SANSANSPVNMPTTGPNLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

30 The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23 (internal identification number 76-4-1-G5-FL1). This cDNA falls into the

"EST-ext" category described above and encodes the signal peptide ILSTVTALTFAXA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 (internal identification number 51-3-3-B10-FL3) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having a von Heijne score of 10.7.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the stored materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the cDNA insertion. The PCR product which corresponds to the cDNA can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The polypeptides encoded by the extended cDNAs may be screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at <http://expasy.hcuge.ch/sprot/prosite.html>). Prosite_convert and prosite_scan programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) may be used to find signatures on the extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence may be assessed by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins may be used as an index. Every pattern for which the ratio is greater than 20% (one hit on shuffled proteins for 5 hits on native proteins) may be skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffled) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5' ESTs. Example 29 below provides examples of such methods.

EXAMPLE 29

Methods for Obtaining cDNAs which include the Entire Coding Region and the Authentic 5'End of the Corresponding mRNA

A full length cDNA library can be made using the strategies described in Examples 13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-dT primer. For instance, the oligonucleotide of SEQ ID NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art. Such cDNA or genomic DNA libraries may be used to isolate extended cDNAs obtained from 5' EST or nucleic acids homologous to extended cDNAs or 5' EST as follows. The cDNA library or genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA using conventional techniques. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises at least 20 to 30 consecutive

nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated
5 herein by reference. The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. A probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA is labeled with a detectable label
10 such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises 20 to 30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

15 Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, *in vitro* transcription, and non radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic
20 DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAs having different levels of homology to the probe can be identified and isolated as described below.

25

1. Identification of Extended cDNA or Genomic cDNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the
30 following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

5 If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA, 50% formamide. The formulas for
10 SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or
15 genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the T_m . Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50%
20 formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room
25 temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5' ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or
30 other conventional techniques.

2. Obtention of Extended cDNA or Genomic cDNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology Between the Obtained Extended cDNAs and the Labeled Probe

If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may be further determined using BLAST2N; parameters may be adapted depending on the sequence length and degree of homology studied. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95%

nucleic acid homology to the extended cDNA or 5'EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5'EST from which the probe was derived.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5'EST from which the probe was derived.

In addition to the above described methods, other protocols are available to obtain extended cDNAs using 5' ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 38-305. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of SEQ ID NOs 38-305. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the sequences of SEQ ID NOs 38-305. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 38-305. If it is desired to obtain extended

cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as
5 described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequence of the 5'EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5'EST and reverse transcribing the hybridized primer to make a first
10 cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5'EST. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the 5'EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary
15 to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may
20 be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described in *Current*
25 *Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989, the entire disclosures of which are incorporated herein by reference.

Alternatively, procedures such as the one described in Example 29 may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended
30 cDNAs are prepared from mRNA and cloned into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by

treatment with an endonuclease, such as the Gene II product of the phage F1, and an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993). A biotinylated oligonucleotide comprising the sequence of a 5' EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5' EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5' EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5' EST sequence are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992). Thereafter, the resulting phagemids containing the 5' EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST sequence. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs containing the 5' EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the mature protein remaining after the signal peptide is cleaved off may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5' ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to express the encoded secreted proteins or portions thereof as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30**Expression of the Proteins Encoded by the Genes Corresponding to 5' ESTs or Portions Thereof**

To express the proteins encoded by the genes corresponding to 5' ESTs (or portions thereof), full length cDNAs containing the entire protein coding region or extended cDNAs containing sequences adjacent to the 5' ESTs (or portions thereof) are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767, incorporated herein by this reference.

The cDNA cloned into the expression vector may encode the entire protein (*i.e.* the signal peptide and the mature protein), the mature protein (*i.e.* the protein created by cleaving the signal peptide off), only the signal peptide or any other portion thereof.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5' ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the polyA signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the

polyA signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector
5 includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of the corresponding cDNA 3' primer,
10 taking care to ensure that the extended cDNA is positioned with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1 containing a poly A signal and prepared for this ligation (blunt/BglII).

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life
15 Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 µg/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described
20 above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the
25 proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques familiar to those skilled in the art such as
30 Coomassie blue or silver staining or using antibodies against the protein encoded by the extended cDNA.

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5' EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5' EST, extended cDNA, or portion thereof.

5 Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5' EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band
10 corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

 Alternatively, if the protein expressed from the above expression vectors does not
15 contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector
20 without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

 The protein encoded by the extended cDNA may be purified using standard
25 immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then
30 released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies, the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β -globin or a nickel binding polypeptide. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β -globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, (*Basic Methods in Molecular Biology*, Davis, Dibner, and Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro* translation systems such as the *In vitro* ExpressTM Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 31 below. It will be appreciated that a plurality of proteins expressed from these cDNAs may be included in a panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are cloned into expression vectors such as those described in Example 30. The proteins are purified by size, charge, immunochromatography or other techniques familiar to those skilled

in the art. Following purification, the proteins are labeled using techniques known to those skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled proteins may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein are incubated along with the labeled protein. The amount of labeled protein bound to the cell surface decreases as the amount of competitive unlabeled protein increases. As a control, various amounts of an unlabeled protein unrelated to the labeled protein is included in some binding reactions. The amount of labeled protein bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The secreted proteins encoded by the extended cDNAs or portions thereof made according to Examples 27-29 may be evaluated to determine their physiological activities as described below.

EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine,

Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein encoded by the extended cDNAs is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,

DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M⁺ (preB M⁺), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references, which are incorporated herein by reference: *Current Protocols in Immunology*, Ed. by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al.* *J. Immunol.* 137:3494-3500, 1986.; Bertagnolli *et al.*, *J. Immunol.* 145:1706-1712, 1990.; Bertagnolli *et al.*, *Cell. Immunol.* 133:327-341, 1991; Bertagnolli, *et al.*, *J. Immunol.* 149:3778-3783, 1992; Bowman *et al.*, *J. Immunol.* 152:1756-1761, 1994.

10 In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology*, *supra* 1:3.12.1-3.12.14; and Schreiber In *Current Protocols in Immunology*, *supra* 1 : 6.8.1-6.8.8.

The proteins encoded by the cDNAs may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references, which are incorporated herein by reference: Bottomly *et al.*, In *Current Protocols in Immunology*, *supra* 1 : 6.3.1-6.3.12.; deVries *et al.*, *J. Exp. Med.* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 36:690-692, 1988; Greenberger *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology*, *supra* 1 : 6.6.1-6.6.5; Smith *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Bennett *et al.*, in *Current Protocols in Immunology supra* 1 : 6.15.1; Ciarletta *et al.*, In *Current Protocols in Immunology. supra* 1 : 6.13.1.

The proteins encoded by the cDNAs may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in *Current Protocols in Immunology supra*; Weinberger *et al.*, *Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur. J. Immun.* 11:405-411, 1981; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988.

Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Activity as Immune System Regulators

The proteins encoded by the cDNAs may also be evaluated for their effects as immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in Immunology*, Coligan *et al.*, Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann *et al.*, *J. Immunol.* 128:1968-1974, 1982; Handa *et al.*, *J. Immunol.* 135:1564-1572, 1985; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988; Bowman *et al.*, *J. Virology* 61:1992-1998; Bertagnolli *et al.*, *Cell. Immunol.* 133:327-341, 1991; Brown *et al.*, *J. Immunol.* 153:3079-3092, 1994.

The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; Mond *et al.* in *Current Protocols in Immunology*, 1 : 3.8.1-3.8.16, *supra*.

The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays

for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in *Current Protocols in Immunology, supra*; Takai *et al.*, *J. Immunol.* **137**:3494-3500, 1986; Takai *et al.*, *J. Immunol.* **140**:508-512, 1988; Bertagnolli *et al.*, *J. Immunol.* **149**:3778-3783, 1992.

5 The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Guery *et al.*, *J. Immunol.* **134**:536-544, 1995; Inaba *et al.*, *J. Exp. Med.* **173**:549-559, 1991; Macatonia *et al.*, *J. Immunol.* **154**:5071-5079, 1995; Porgador *et al.*, *J. Exp. Med.* **182**:255-260, 1995; Nair *et al.*, *J. Virol.* **67**:4062-4069, 10 1993; Huang *et al.*, *Science* **264**:961-965, 1994; Macatonia *et al.*, *J. Exp. Med.* **169**:1255-1264, 1989; Bhardwaj *et al.*, *Journal of Clinical Investigation* **94**:797-807, 1994; and Inaba *et al.*, *J. Exp. Med.* **172**:631-640, 1990.

 The proteins encoded by the cDNAs may also be evaluated for their influence on the 15 lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Darzynkiewicz *et al.*, *Cytometry* **13**:795-808, 1992; Gorczyca *et al.*, *Leukemia* **7**:659-670, 1993; Gorczyca *et al.*, *Cancer Res.* **53**:1945-1951, 1993; Itoh *et al.*, *Cell* **66**:233-243, 1991; Zacharchuk, *J. Immunol.* **145**:4037-4045, 1990; Zamai *et al.*, *Cytometry* **14**:891-20 897, 1993; Gorczyca *et al.*, *Int. J. Oncol.* **1**:639-648, 1992.

 The proteins encoded by the cDNAs may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references, which are incorporated herein by references: Antica *et al.*, *Blood* 25 **84**:111-117, 1994; Fine *et al.*, *Cell. Immunol.* **155**:111-122, 1994; Galy *et al.*, *Blood* **85**:2770-2778, 1995; Toki *et al.*, *Proc. Nat. Acad. Sci. USA* **88**:7548-7551, 1991.

 Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of 30 various immune deficiencies and disorders (including severe combined immunodeficiency), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well

as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein encoded
5 by extended cDNAs derived from the 5' ESTs of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plamodium and various fungal infections such as candidiasis. Of course, in this regard, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

10 Alternatively, proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease
15 and autoimmune inflammatory eye disease. Such a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma. (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein encoded by
20 extended cDNAs derived from the 5' ESTs of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses either up or down.

Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of
25 activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and
30 persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be

demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792, 1992 and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105, 1992. In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/pr/pr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *supra*, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, antiviral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention or together with a stimulatory form of a soluble peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention and reintroducing the *in vitro* primed T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain and β_2 microglobulin or an MHC class II α chain and an MHC class II β chain to thereby express MHC class I or MHC class II proteins on the cell surface, respectively. Expression of the appropriate MHC class I or class II molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these immune system regulator proteins or nucleic acids regulating the expression of

such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

5 Assaying the Proteins Expressed from Extended cDNAs
 or Portions Thereof for Hematopoiesis Regulating Activity

 The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity
10 are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Johansson *et al.* *Cell. Biol.* 15:141-151, 1995; Keller *et al.*, *Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

 The proteins encoded by the extended cDNAs or portions thereof may also be
15 evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Freshney, Methylcellulose Colony Forming Assays, in *Culture of Hematopoietic Cells*, Freshney, *et al.* Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al.*, *Proc. Natl. Acad.*
20 *Sci. USA* 89:5907-5911, 1992; McNiece and Briddell, in *Culture of Hematopoietic Cells*, *supra*; Neben *et al.*, *Exp. Hematol.* 22:353-359, 1994; Ploemacher and Cobblestone In *Culture of Hematopoietic Cells*, *supra* 1-21, Spooncer *et al.*, in *Culture of Hematopoietic Cells*, *supra* 163-179 and Sutherland in *Culture of Hematopoietic Cells*, *supra*. 139-162.

 Those proteins which exhibit hematopoiesis regulatory activity may then be
25 formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoeisis is beneficial, such as in the treatment of myeloid or lymphoid cell deficiencies. Involvement in regulating hematopoiesis is indicated even by marginal biological activity in support of colony forming cells or of factor-dependent cell lines. For example, proteins supporting the growth and proliferation of erythroid progenitor cells alone or in combination
30 with other cytokines, indicates utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors

and/or erythroid cells. Proteins supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) may be useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression. Proteins supporting the growth and proliferation of megakaryocytes and consequently of platelets allows prevention or treatment of various platelet disorders such as thrombocytopenia, and generally may be used in place of or complementary to platelet transfusions. Proteins supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells may therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in vivo* or *ex vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding hematopoiesis regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Tissue Growth

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491, which are incorporated herein by reference.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112, Maibach and Rovee, eds., Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol.* 71:382-84, 1978, which are incorporated herein by reference.

Those proteins which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of bone-forming cell progenitors. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein encoded by extended cDNAs derived from the 5' ESTs of the present invention is tendon/ligament formation. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue

formation induced by a composition encoded by extended cDNAs derived from the 5' ESTs of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions encoded by extended cDNAs derived from the 5' ESTs of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

5 A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

10 A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding tissue growth regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

15

EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Reproductive Hormones

20 The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Vale *et al.*, *Endocrinol.* **91**:562-572, 1972; Ling *et al.*, *Nature* **321**:779-782, 1986; Vale *et al.*, *Nature* **321**:776-779, 1986; Mason *et al.*, *Nature* **318**:659-663, 1985; Forage *et al.*,
25 *Proc. Natl. Acad. Sci. USA* **83**:3091-3095, 1986, Chapter 6.12 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Taub *et al.*, *J. Clin. Invest.* **95**:1370-1376, 1995; Lind *et al.*, *APMIS* **103**:140-146, 1995; Muller *et al.*, *Eur. J. Immunol.* **25**:1744-1748; Gruber *et al.*, *J. Immunol.* **152**:5860-5867, 1994; Johnston *et al.*, *J Immunol.* **153**:1762-1768, 1994.

30 Those proteins which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in

which regulation of reproductive hormones are beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of FSH. Thus, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885, the disclosure of which is incorporated herein by reference. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding reproductive hormone regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 37

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Chemotactic/Chemokinetic Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins

provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

5 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell
10 chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of
15 cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by Coligan, Kruisbeek, Margulies, Shevach and Strober, Pub. Greene Publishing Associates and Wiley-Interscience, Chapter 6.12: 6.12.1-6.12.28; Taub *et al.*, *J. Clin. Invest.* **95**:1370-1376, 1995;
20 Lind *et al.*, *APMIS* **103**:140-146, 1995; Mueller *et al.*, *Eur. J. Immunol.* **25**:1744-1748; Gruber *et al.*, *J. Immunol.* **152**:5860-5867, 1994; Johnston *et al.* *J. Immunol.*, **153**:1762-1768, 1994.

EXAMPLE 38

25 Assaying the Proteins Expressed from Extended cDNAs or
 Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are
30 incorporated herein by reference: Linet *et al.*, *J. Clin. Pharmacol.* **26**:131-140, 1986; Burdick

et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79, 1991; Schaub, *Prostaglandins* 35:467-474, 1988.

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in more detail below, genes encoding blood clotting activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 39

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 7. 7.28.1-7.28.22 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Takai *et al.*, *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160, 1989; Stoltenborg *et al.*, *J. Immunol. Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995; Gyuris *et al.*, *Cell* 75:791-803, 1993.

For example, the proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include,

without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
5 recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions. Alternatively,
10 as described in more detail below, genes encoding proteins involved in receptor/ligand interactions or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 40

15 Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof
for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Alternatively, as described in more detail below, genes encoding anti-inflammatory activity proteins or nucleic

acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 41

5 Assaying the Proteins Expressed from Extended cDNAs or
 Portions Thereof for Tumor Inhibition Activity

 The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other
10 anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or
15 inhibiting factors, agents or cell types which promote tumor growth. Alternatively, as described in more detail below, genes tumor inhibition activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

20 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or
25 body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral
30 characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors;

providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, genes encoding proteins involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 42

Identification of Proteins which Interact with

Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by cDNAs derived from the 5' ESTs or fragments thereof, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the kit which is incorporated herein by reference, the the cDNAs derived from 5' ESTs, or fragments thereof, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which might interact with the polypeptides encoded by the extended cDNAs or portions thereof are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins which interact with the polypeptide encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* 283: 83-99, 1997, and in U.S. Patent No. 5,654,150, the disclosure of which is incorporated herein by reference, may be used for identifying molecules which interact with the polypeptides encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed
5 on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a
10 desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended cDNAs can be found by a variety of additional techniques. In one method, affinity columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains
15 chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al.*, *Electrophoresis* 18:588-598,
20 1997, the disclosure of which is incorporated herein by reference. Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Proteins interacting with polypeptides encoded by extended cDNAs or portions thereof can also be screened by using an Optical Biosensor as described in Edwards and
25 Leatherbarrow, *Analytical Biochemistry* 246:1-6, 1997, the disclosure of which is incorporated herein by reference. The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or
30 low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethyl dextran matrix) and a sample of test molecules is placed in contact with

the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can
5 be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

10 In other methods, a target protein is immobilized and the test population is a collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the microdialysis coupled to HPLC method described by Wang *et al.*, *Chromatographia* 44:205-208, 1997 or the affinity capillary electrophoresis
15 method described by Busch *et al.*, *J. Chromatogr.* 777:311-328, 1997, the disclosures of which are incorporated herein by reference can be used.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those
20 specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the cDNAs or portions thereof may be used to generate
25 antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may capable of binding a full length protein encoded by a cDNA derived from a 5' EST, a mature protein (*i.e.* the protein generated by cleavage of the signal peptide) encoded by a cDNA derived from a 5' EST, or a signal peptide encoded by a cDNA derived from a 5' EST. Alternatively, the antibodies may be
30 capable of binding fragments of at least 10 amino acids of the proteins encoded by the above cDNAs. In some embodiments, the antibodies may be capable of binding fragments of at

least 15 amino acids of the proteins encoded by the above cDNAs. In other embodiments, the antibodies may be capable of binding fragments of at least 25 amino acids of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the proteins encoded by the above cDNAs. In further embodiments, the antibodies may be capable of binding fragments of at least 40 amino acids of the proteins encoded by the above cDNAs.

EXAMPLE 43

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few $\mu\text{g/ml}$. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* 256:495, 1975 or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419, 1980, the disclosure of which is incorporated herein by reference and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis *et al.* in *Basic Methods in Molecular Biology*

Elsevier, New York. Section 21-2, the disclosure of which is incorporated herein by reference.

2. Polyclonal Antibody Production by Immunization

5 Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less
10 immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, *et al*, *J. Clin. Endocrinol. Metab.* **33**:988-991 (1971), the disclosure of which is incorporated herein by reference.

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier
20 (ed) Blackwell (1973), the disclosure of which is incorporated herein by reference. Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980), the
25 disclosure of which is incorporated herein by reference.

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in
30 therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

V. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

1. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Isolation, Diagnostic and Forensic Procedures

EXAMPLE 44

Preparation of PCR Primers and Amplification of DNA

The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see *Molecular Cloning to Genetic Engineering*, White Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa 1997, the disclosure of which is incorporated herein by reference. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation,

hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 45

5

Use of 5' ESTs as Probes

Probes derived from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), including full length cDNAs or genomic sequences, may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

PCR primers made as described in Example 44 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 46-50 below. Such analyses may utilize detectable probes or primers based on the sequences of the the 5' ESTs or of cDNAs or genomic DNAs isolated using the 5' ESTs.

30

EXAMPLE 46Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the 5' ESTs of Example 25, or cDNAs or genomic DNAs isolated therefrom as described above, is then utilized in accordance with Example 44 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 47Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of 5'EST sequences from Example 25, or cDNA or genomic DNA sequences obtainable therefrom. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 44. Each of these DNA segments is sequenced, using the methods set forth in Example 46. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 48**Southern Blot Forensic Identification**

The procedure of Example 47 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65), the disclosure of which is incorporated herein by reference.

A panel of probes based on the sequences of 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*, supra). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 49Dot Blot Identification Procedure

Another technique for identifying individuals using the 5' EST sequences disclosed herein utilizes a dot blot hybridization technique.

5 Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10, preferably 50 sequences from the 5' ESTs or cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P^{32} using polynucleotide kinase
10 (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis *et al.*, *supra*). The ^{32}P labeled DNA fragments are sequentially hybridized with successively stringent conditions to
15 detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al.*, *Proc. Natl. Acad. Sci. USA* **82**(6):1585-1588, 1985) which is hereby incorporated by reference. A unique pattern of dots distinguishes one individual from another individual.

20 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30
25 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 50 below provides a representative alternative
30 fingerprinting procedure in which the probes are derived from 5'EST.

EXAMPLE 50Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of 5'EST using commercially available oligonucleotide services such as Genset, Paris, France.

5 Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into

10 wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with ^{32}P . The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray

15 film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The proteins encoded by the extended cDNAs may also be used to generate

20 antibodies as explained in Examples 30 and 43 in order to identify the tissue type or cell species from which a sample is derived as described in example 51.

EXAMPLE 51Identification of Tissue Types or Cell Species by Means of

25 Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations according to Examples 30 and 43 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts

30 of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. Immunohistochemical techniques

10 Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, Chap. 26 in: *Basic and Clinical Immunology*, 3rd Ed. Lange, Los Altos, California, 1980, or Rose, *et al.*, Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980), the disclosures of which are incorporated herein by reference.

15 A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I , and detected by overlaying the antibody treated preparation with photographic emulsion.

20 Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μm , unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative

control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker
5 developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are
10 commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

B. Identification of tissue specific soluble proteins

15 The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

20 A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

25 A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, *et al.*, Section 19-2 in: *Basic Methods in Molecular Biology*, Leder ed., Elsevier, New York, 1986, the disclosure of which is incorporated herein by reference, using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be
30 detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5

to 55 μ l, and containing from about 1 to 100 μ g protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al.*, *supra* Section 19-3. One set of nitrocellulose
5 blots is stained with Coomassie blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 43. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

10 In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule,
15 which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences
20 identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

In addition to their applications in forensics and identification, 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be mapped to their chromosomal
25 locations. Example 52 below describes radiation hybrid (RH) mapping of human chromosomal regions using 5'ESTs. Example 53 below describes a representative procedure for mapping an 5' EST to its location on a human chromosome. Example 54 below describes mapping of 5' ESTs on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH). Those skilled in the art will appreciate that the method of
30 Examples 52-54 may also be used to map cDNAs or genomic DNAs obtainable from the 5' ESTs to their chromosomal locations.

2. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Chromosome Mapping

EXAMPLE 52

Radiation hybrid mapping of 5'ESTs to the human genome

5 Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human
10 genome. This technique is described by Benham *et al.*, *Genomics* 4:509-517, 1989; and Cox *et al.*, *Science* 250:245-250, 1990, the entire contents of which are hereby incorporated by reference. The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering 5'EST. In this approach, the frequency of breakage between
15 markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler *et al.*, *Science* 274:540-546, 1996, hereby incorporated by reference).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH)
20 and thymidine kinase (TK) (Foster *et al.*, *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* 14:574-584, 1992) and 13 loci on the
25 long arm of chromosome 5 (Warrington *et al.*, *Genomics* 11:701-708, 1991).

EXAMPLE 53

Mapping of 5'ESTs to Human Chromosomes using PCR techniques

5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be assigned to
30 human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the 5' ESTs (or cDNAs or genomic DNAs obtainable

therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich in *PCR Technology, Principles and Applications*
5 *for DNA Amplification*, Freeman and Co., New York, 1992, the disclosure of which is incorporated herein by reference.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase,
10 and 1 μ Cu of a 32 P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance
15 between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets
20 of human chromosomes for the presence of a given 5' EST (or cDNA or genomic DNA obtainable therefrom). DNA is isolated from the somatic hybrids and used as starting templates for PCR reactions using the primer pairs from the 5' EST (or cDNA or genomic DNA obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the 5' EST (or cDNA or genomic DNA obtainable
25 therefrom) will yield an amplified fragment. The 5' EST (or cDNA or genomic DNA obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that 5'EST (or cDNA or genomic DNA obtainable therefrom). For a review of techniques
30 and analysis of results from somatic cell gene mapping experiments, see Ledbetter *et al.*, *Genomics* 6:475-481, 1990, the disclosure of which is incorporated herein by reference.

EXAMPLE 54**Mapping of Extended 5' ESTs to Chromosomes Using Fluorescence *In Situ*****Hybridization**

Fluorescence in situ hybridization allows the 5'EST (or cDNA or genomic DNA
5 obtainable therefrom) to be mapped to a particular location on a given chromosome. The
chromosomes to be used for fluorescence in situ hybridization techniques may be obtained
from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an 5'EST (or cDNA or
genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif *et al.* (*Proc.*
10 *Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990), the disclosure of which is incorporated herein
by reference. Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-
stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured
for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μ M) is added for 17
h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1
15 μ g/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in
RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in
three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide
and air dried. The 5'EST (or cDNA or genomic DNA obtainable therefrom) is labeled with
biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda
20 Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia,
Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in
hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated
salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μ g/ml), rinsed
25 three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are
denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The
slides are treated with proteinase K (10 μ g/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C
for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the
slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid
30 chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is
detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin

and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra.*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots
5 on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given chromosome.

Once the 5'EST (or cDNA or genomic DNA obtainable therefrom) have been
10 assigned to particular chromosomes using the techniques described in Examples 52-54 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 55

15 Use of 5'EST to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial
20 chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Nagaraja *et al.*, *Genome Research* 7:210-222, 1997, the disclosure of which is incorporated herein by reference. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector.
25 The YAC inserts are screened using PCR or other methods to determine whether they include the 5'EST (or cDNA or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the 5'EST (or cDNA or genomic DNA obtainable therefrom), the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome
30 or in the region from which the 5'EST (or cDNA or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the

location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be obtained.

5

As described in Example 56 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

10 3. Use of 5'ESTs or Sequences Obtained Therefrom or Fragments Thereof in Gene Identification

EXAMPLE 56

Identification of genes associated with hereditary diseases or drug response

15 This example illustrates an approach useful for the association of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) with particular phenotypic characteristics. In this example, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) is used as a test probe to associate that 5'EST (or cDNA or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

20 5'ESTs (or cDNA or genomic DNA obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 52 and 53 or other techniques known in the art. A search of Mendelian Inheritance in Man (McKusick in *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be a very gene rich
25 region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this 5'EST (or cDNA or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

30 Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the 5'EST (or cDNA or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the

patients. 5'ESTs (or cDNA or genomic DNA obtainable therefrom) that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the 5'EST may be responsible for the genetic disease.

VI. Use of 5'EST (or cDNA or Genomic DNA Obtainable Therefrom) to Construct Vectors

The present 5'ESTs (or cDNA or genomic DNA obtainable therefrom) may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 57 below.

1. Construction of Secretion Vectors

EXAMPLE 57

Construction of Secretion Vectors

The secretion vectors include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from a 5' EST (or cDNAs or genomic DNAs obtainable therefrom) is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the 5' EST (or cDNA or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The 5' ESTs may also be used to clone sequences located upstream of the 5' ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 58 describes a method for cloning sequences upstream of the extended cDNAs or 5' ESTs.

2. Identification of Upstream Sequences With Promoting or Regulatory Activities

10

EXAMPLE 58

Use of Extended cDNAs or 5' ESTs to Clone Upstream Sequences from Genomic DNA

Sequences derived from extended cDNAs or 5' ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions (which are incorporated herein by reference) using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for the extended cDNA or 5' EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5 ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of Mg(OAc)₂, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (7 cycles) / 2 sec - 94°C, 3 min - 67°C (32 cycles) / 5 min - 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR

reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adaptor, and is provided with the GenomeWalker™ kit.

- 5 The second nested primer is specific for the particular extended cDNA or 5' EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (6 cycles) / 2 sec - 94°C, 3 min - 67°C (25 cycles) / 5
10 min - 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

- Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated
15 oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5' EST sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and
20 converted into double stranded DNA using a primer specific for the extended cDNA or 5' EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5' EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

- 25 Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5' ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

- 30 In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example .

EXAMPLE 59Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the extended cDNAs or 5' ESTs are cloned into
5 a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, p β gal-
Basic, p β gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech.
Briefly, each of these promoter reporter vectors include multiple cloning sites positioned
upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline
phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the
10 extended cDNAs or 5' ESTs are inserted into the cloning sites upstream of the reporter gene
in both orientations and introduced into an appropriate host cell. The level of reporter protein
is assayed and compared to the level obtained from a vector which lacks an insert in the
cloning site. The presence of an elevated expression level in the vector containing the insert
with respect to the control vector indicates the presence of a promoter in the insert. If
15 necessary, the upstream sequences can be cloned into vectors which contain an enhancer for
augmenting transcription levels from weak promoter sequences. A significant level of
expression above that observed with the vector lacking an insert indicates that a promoter
sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the
20 results of the above described determination of expression patterns of the extended cDNAs
and ESTs. For example, if the expression pattern analysis indicates that the mRNA
corresponding to a particular extended cDNA or 5' EST is expressed in fibroblasts, the
promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by
25 constructing nested deletions in the upstream DNA using conventional techniques such as
Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter
reporter vector to determine whether the deletion has reduced or obliterated promoter
activity. In this way, the boundaries of the promoters may be defined. If desired, potential
individual regulatory sites within the promoter may be identified using site directed
30 mutagenesis or linker scanning to obliterate potential transcription factor binding sites within
the promoter individually or in combination. The effects of these mutations on transcription

levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 60

5 Cloning and Identification of Promoters

Using the method described in Example 58 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was
10 obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and
15 GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start
20 sites using the computer program MatInspector release 2.0, August 1996.

Table VII describes the transcription factor binding sites present in each of these promoters. The columns labeled matrice provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on
25 which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site
30 found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium.

- 5 The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard
- 10 cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

- The promoters and other regulatory sequences located upstream of the extended
- 15 cDNAs or 5' ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For example, if a promoter which confers a high level of expression in
- 20 muscle is desired, the promoter sequence upstream of an extended cDNA or 5' EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

- Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able
- 25 to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 58-60, proteins which interact with the promoter may be identified as described in Example 61 below.

EXAMPLE 61

Identification of Proteins Which Interact with Promoter Sequences, Upstream

Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1), the disclosure of which is incorporated herein by reference. Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to

select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression
5 vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNase protection analysis.

VII. Use of 5' ESTs (or cDNAs or Genomic DNAs Obtainable Therefrom) in Gene 10 Therapy

The present invention also comprises the use of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies as described in Examples 62 and 63 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the
15 expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense
20 sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

EXAMPLE 62

25 Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom). The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular
30 duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et*

al., *Ann. Rev. Biochem.* 55:569-597, 1986; and Izant and Weintraub, *Cell* 36:1007-1015, 1984, which are hereby incorporated by reference.

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, 1991, which is hereby incorporated by reference.

Various types of antisense oligonucleotides complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026, hereby incorporated by reference, are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, hereby incorporated by reference, are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, hereby incorporated by reference, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages,

wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, incorporated by reference, may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefore. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2, hereby incorporated by reference are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732, hereby incorporated by reference, is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection, transfection or h-region-mediated import using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors,

vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between 1×10^{-10} M to 1×10^{-4} M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al.*, *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at

homopurine:homopyrimidine sequences. Thus, both types of sequences from the 5'EST or from the gene corresponding to the 5'EST are contemplated within the scope of this invention.

5

EXAMPLE 63

Preparation and Use of Triple Helix Probes

The sequences of the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following
10 identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis,
15 such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using
20 techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The
25 cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 56.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 62
30 at a dosage calculated based on the *in vitro* results, as described in Example 62.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin *et al.*, *Science* 245:967-971, 1989, which is hereby incorporated by this reference.

EXAMPLE 64

Use of cDNAs Obtained Using the 5' ESTs to Express an Encoded Protein in a Host

Organism

The cDNAs obtained as described above using the 5' ESTs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

EXAMPLE 65

Use of Signal Peptides Encoded by 5' ESTs or Sequences obtained Therefrom
to Import Proteins Into Cells

5 The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or extended cDNAs derived from SEQ ID NOs: 38-305 may also be used as a carrier to import a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol. Chem.*, **270**: 14225-14258, 1995; Du *et al.*, *J. Peptide Res.*, **51**: 235-243, 1998; Rojas *et al.*, *Nature Biotech.*, **16**: 370-375, 1998).

10 When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA
15 sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

20 This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, **271**: 5305-5308, 1996; Rojas *et al.*, *J. Biol. Chem.*, **271**: 27456-27461, 1996; Liu *et al.*, *Proc. Natl. Acad. Sci. USA*,
25 **93**: 11819-11824, 1996; Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, **234**: 675-680, 1997).

Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

30 Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form

triple helixes, as described in examples 62 and 63 respectively, in order to inhibit processing and/or maturation of a target cellular RNA.

As discussed above, the cDNAs or portions thereof obtained using the 5' ESTs of the present invention can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* 75:791-803, 1993, the disclosure of which is hereby incorporated by reference) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins

involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, Fritsch and Maniatis eds., 1989, and *Methods in Enzymology: Guide to Molecular Cloning Techniques*, Academic Press, Berger and Kimmel eds., 1987.

10 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid
15 preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

 Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the
20 disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. All documents cited herein are incorporated herein by reference in their entirety.

Step	Search characteristic		Selection Characteristics		
	Program	Strand	Parameters	Identity (%)	Length (bp)
miscellaneous	blastn	both	S=61 X=16	90	17
tRNA	fasta	both	-	80	60
rRNA	blastn	both	S=108	80	40
mtRNA	blastn	both	S=108	80	40
Prokaryotic	blastn	both	S=144	90	40
Fungal	blastn	both	S=144	90	40
Alu	fasta*	both	-	70	40
L1	blastn	both	S=72	70	40
Repeats	blastn	both	S=72	70	40
Promoters	blastn	top	S=54 X=16	90	15†
Vertebrate	fasta*	both	S=108	90	30
ESTs	blastn	both	S=108 X=16	90	30
Proteins	blastx‡	top	E = 0.001	-	-

Table 1: Parameters used for each step of EST analysis

- * use "Quick Fast" Database scanner
- † alignment further constrained to begin closer than 10bp to EST's end
- ‡ using BLOSUM62 substitution matrix

TABLE II

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID38	new	15.8	Heart	25-13-1-H10-PU
ID39	new	14	Fetal kidney	58-47-2-B11-PU
ID40	new	12.3	Dystrophic muscle	29-3-3-H8-PU
ID41	new	12.2	Fetal kidney	58-4-2-A3-PU
ID42	new	11.9	Kidney	21-10-4-G1-PU
ID43	new	11.3	Fetal kidney	58-27-3-B10-PU
ID44	new	10.7	Fetal kidney	58-35-2-F10-PU
ID45	new	10.7	Fetal kidney	58-37-2-G10-PU
ID46	new	10.6	Dystrophic muscle	29-11-1-C11-PU
ID47	new	10	Fetal kidney	58-20-4-G7-PU
ID48	new	10	Fetal kidney	58-2-4-E9-PU
ID49	new	9.6	Fetal kidney	58-37-3-D8-PU
ID50	new	9.5	Fetal kidney	58-46-1-F1-PU
ID51	new	9.2	Dystrophic muscle	29-9-4-D8-PU
ID52	new	9.2	Muscle	27-10-4-C6-PU
ID53	new	8.3	Heart	67-5-4-H9-PU
ID54	new	8.1	Fetal kidney	58-4-3-H4-PU
ID55	new	8	Muscle	27-16-3-D12-PU
ID56	new	7.9	Fetal kidney	58-54-2-C2-PU
ID57	new	7.9	Heart	25-9-3-A3-PU
ID58	new	7.9	Dystrophic muscle	29-11-3-F1-PU
ID59	new	7.9	Fetal kidney	58-32-3-G6-PU
ID60	new	7.8	Fetal kidney	58-22-2-H8-PU
ID61	new	7.8	Fetal kidney	58-2-4-H4-PU
ID62	new	7.8	Heart	67-4-3-G3-PU
ID63	new	7.8	Fetal kidney	58-24-1-G11-PU
ID64	new	7.7	Fetal kidney	58-19-3-H1-PU
ID65	new	7.5	Fetal kidney	58-45-4-B11-PU
ID66	new	7.3	Fetal kidney	58-44-2-D3-PU
ID67	new	7.2	Dystrophic muscle	29-3-3-E7-PU
ID68	new	7.1	Dystrophic muscle	29-12-3-A3-PU
ID69	new	7.1	Fetal kidney	58-14-2-B3-PU
ID70	new	7.1	Fetal kidney	58-10-3-D12-PU
ID71	new	7	Fetal kidney	58-6-2-E5-PU
ID72	new	7	Dystrophic muscle	29-7-1-C1-PU
ID73	new	6.9	Fetal kidney	58-26-4-A12-PU
ID74	new	6.9	Fetal kidney	58-7-2-H9-PU
ID75	new	6.9	Fetal kidney	58-14-2-D5-PU
ID76	new	6.7	Fetal kidney	58-3-4-E1-PU
ID77	new	6.7	Fetal kidney	58-43-4-G3-PU
ID78	new	6.7	Fetal kidney	58-11-1-G10-PU
ID79	new	6.6	Fetal kidney	58-4-4-G2-PU
ID80	new	6.6	Fetal kidney	58-41-3-D6-PU
ID81	new	6.6	Heart	25-8-2-H10-PU
ID82	new	6.5	Muscle	27-18-4-E5-PU
ID83	new	6.4	Dystrophic muscle	29-4-1-G6-PU
ID84	new	6.4	Muscle	27-10-2-B1-PU
ID85	new	6.4	Fetal kidney	58-38-1-E5-PU
ID86	new	6.3	Muscle	27-4-3-D9-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID87	new	6.3	Fetal kidney	58-53-1-G1-PU
ID88	new	6.3	Fetal kidney	58-7-3-F6-PU
ID89	new	6.3	Heart	25-7-2-B12-PU
ID90	new	6.1	Fetal kidney	58-16-3-E11-PU
ID91	new	6	Fetal kidney	58-15-4-C2-PU
ID92	new	6	Fetal kidney	58-34-3-A9-PU
ID93	new	5.9	Fetal kidney	58-16-1-E1-PU
ID94	new	5.9	Fetal kidney	58-4-3-E6-PU
ID95	new	5.9	Fetal kidney	58-37-3-B11-PU
ID96	new	5.9	Fetal kidney	58-35-3-C6-PU
ID97	new	5.8	Fetal kidney	58-35-1-D9-PU
ID98	new	5.8	Fetal kidney	58-26-3-B2-PU
ID99	new	5.7	Fetal kidney	58-48-1-F8-PU
ID100	new	5.7	Fetal kidney	58-27-4-A6-PU
ID101	new	5.7	Fetal kidney	58-26-3-D1-PU
ID102	new	5.7	Muscle	27-19-4-B4-PU
ID103	new	5.6	Fetal kidney	58-23-3-B2-PU
ID104	new	5.5	Heart	25-1-2-C1-PU
ID105	new	5.5	Fetal kidney	58-14-3-F10-PU
ID106	new	5.5	Fetal kidney	58-25-1-E11-PU
ID107	new	5.5	Muscle	27-9-4-A10-PU
ID108	new	5.5	Heart	25-4-2-D8-PU
ID109	new	5.4	Fetal kidney	58-29-3-G8-PU
ID110	new	5.4	Fetal kidney	58-4-4-E5-PU
ID111	new	5.4	Fetal kidney	58-24-2-H2-PU
ID112	new	5.4	Muscle	27-11-2-C8-PU
ID113	new	5.4	Fetal kidney	58-41-2-E3-PU
ID114	new	5.3	Muscle	27-22-1-G8-PU
ID115	new	5.3	Dystrophic muscle	29-1-1-C9-PU
ID116	new	5.3	Fetal kidney	58-22-2-A3-PU
ID117	new	5.2	Fetal kidney	58-42-2-G1-PU
ID118	new	5.2	Fetal kidney	58-52-2-E5-PU
ID119	new	5.2	Fetal kidney	58-24-2-G2-PU
ID120	new	5.2	Fetal kidney	58-29-1-A3-PU
ID121	new	5.1	Fetal kidney	58-26-1-G8-PU
ID122	new	5.1	Fetal kidney	58-29-4-G12-PU
ID123	new	5.1	Dystrophic muscle	29-8-3-E8-PU
ID124	new	5.1	Dystrophic muscle	29-3-4-C1-PU
ID125	new	5	Fetal kidney	58-17-2-H1-PU
ID126	new	5	Fetal kidney	58-9-3-E3-PU
ID127	new	5	Muscle	27-19-3-G7-PU
ID128	new	5	Fetal kidney	58-41-3-B4-PU
ID129	new	5	Dystrophic muscle	29-7-4-G7-PU
ID130	new	5	Muscle	27-9-3-D4-PU
ID131	new	4.9	Kidney	21-3-4-C5-PU
ID132	new	4.9	Heart	25-11-2-D6-PU
ID133	new	4.9	Heart	67-7-2-F3-PU
ID134	new	4.8	Fetal kidney	58-4-3-D3-PU
ID135	new	4.8	Fetal kidney	58-49-3-B5-PU
ID136	new	4.8	Fetal kidney	58-28-3-G12-PU
ID137	new	4.7	Fetal kidney	58-53-1-A5-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID138	new	4.7	Fetal kidney	58-3-3-E10-PU
ID139	new	4.7	Fetal kidney	58-8-1-G7-PU
ID140	new	4.6	Fetal kidney	58-23-1-G9-PU
ID141	new	4.6	Fetal kidney	58-21-1-H8-PU
ID142	new	4.6	Fetal kidney	58-54-2-E10-PU
ID143	new	4.6	Fetal kidney	58-46-3-E4-PU
ID144	new	4.6	Fetal kidney	58-6-3-G3-PU
ID145	new	4.6	Fetal kidney	58-41-2-B5-PU
ID146	new	4.6	Dystrophic muscle	29-7-3-F2-PU
ID147	new	4.5	Fetal kidney	58-2-4-G12-PU
ID148	new	4.5	Fetal kidney	58-11-2-G8-PU
ID149	new	4.4	Fetal kidney	58-17-1-C4-PU
ID150	new	4.4	Fetal kidney	58-46-1-G7-PU
ID151	new	4.4	Heart	67-3-2-F4-PU
ID152	new	4.4	Fetal kidney	58-8-4-E12-PU
ID153	new	4.4	Fetal kidney	58-4-2-D9-PU
ID154	new	4.4	Fetal kidney	58-25-1-B5-PU
ID155	new	4.4	Fetal kidney	58-15-1-C10-PU
ID156	new	4.3	Dystrophic muscle	29-4-4-A10-PU
ID157	new	4.3	Fetal kidney	58-32-3-H7-PU
ID158	new	4.3	Kidney	21-4-4-D12-PU
ID159	new	4.3	Fetal kidney	58-45-4-G9-PU
ID160	new	4.3	Fetal kidney	58-1-2-E2-PU
ID161	new	4.2	Fetal kidney	58-25-4-E6-PU
ID162	new	4.2	Fetal kidney	58-36-4-C6-PU
ID163	new	4.2	Dystrophic muscle	29-9-3-D5-PU
ID164	new	4.2	Fetal kidney	58-3-3-B8-PU
ID165	new	4.2	Heart	25-4-4-B4-PU
ID166	new	4.2	Kidney	21-10-3-A3-PU
ID167	new	4.2	Muscle	27-19-4-B5-PU
ID168	new	4.2	Fetal kidney	58-23-3-D10-PU
ID169	new	4.1	Fetal kidney	58-41-1-F8-PU
ID170	new	4.1	Heart	25-7-2-B1-PU
ID171	new	4.1	Fetal kidney	58-53-3-G4-PU
ID172	new	4.1	Fetal kidney	58-52-2-C2-PU
ID173	new	4	Muscle	27-21-4-E12-PU
ID174	new	4	Fetal kidney	58-22-2-B8-PU
ID175	new	4	Fetal kidney	58-9-3-A8-PU
ID176	new	4	Muscle	27-5-4-C10-PU
ID177	new	4	Fetal kidney	58-38-1-G5-PU
ID178	new	4	Fetal kidney	58-34-4-F6-PU
ID179	new	4	Heart	25-1-4-D2-PU
ID180	new	4	Fetal kidney	58-48-2-D6-PU
ID181	new	3.9	Fetal kidney	58-9-3-C10-PU
ID182	new	3.9	Fetal kidney	58-9-4-F2-PU
ID183	new	3.9	Fetal kidney	58-32-3-G3-PU
ID184	new	3.9	Fetal kidney	58-52-1-F6-PU
ID185	new	3.9	Fetal kidney	58-29-1-E1-PU
ID186	new	3.9	Muscle	27-3-4-A3-PU
ID187	new	3.9	Muscle	27-16-3-H2-PU
ID188	new	3.9	Fetal kidney	58-1-3-E1-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID189	new	3.8	Kidney	21-5-4-F10-PU
ID190	new	3.8	Kidney	21-1-3-C9-PU
ID191	new	3.8	Fetal kidney	58-1-2-C7-PU
ID192	new	3.8	Fetal kidney	58-10-3-B6-PU
ID193	new	3.8	Fetal kidney	58-11-4-C8-PU
ID194	new	3.8	Heart	67-6-4-B12-PU
ID195	new	3.8	Fetal kidney	58-7-3-B5-PU
ID196	new	3.8	Fetal kidney	58-46-3-C6-PU
ID197	new	3.7	Dystrophic muscle	29-2-4-D8-PU
ID198	new	3.7	Fetal kidney	58-7-1-D10-PU
ID199	new	3.7	Kidney	21-2-4-A11-PU
ID200	new	3.6	Fetal kidney	58-45-3-B7-PU
ID201	new	3.6	Fetal kidney	58-29-1-D7-PU
ID202	new	3.6	Fetal kidney	58-16-3-B3-PU
ID203	new	3.6	Dystrophic muscle	29-7-3-C3-PU
ID204	new	3.6	Fetal kidney	58-42-3-C2-PU
ID205	new	3.5	Fetal kidney	58-38-3-G8-PU
ID206	new	3.5	Dystrophic muscle	29-6-2-B12-PU
ID207	new	3.5	Fetal kidney	58-8-1-D1-PU
ID208	new	3.5	Fetal kidney	58-24-1-H2-PU
ID209	new	3.5	Fetal kidney	58-41-4-G9-PU
ID210	ext-est-not-vrt	12.7	Muscle	27-22-3-H1-PU
ID211	ext-est-not-vrt	10.5	Fetal kidney	58-29-1-F11-PU
ID212	ext-est-not-vrt	8	Fetal kidney	58-14-2-B12-PU
ID213	ext-est-not-vrt	7.7	Fetal kidney	58-5-1-C4-PU
ID214	ext-est-not-vrt	7.1	Fetal kidney	58-37-4-C7-PU
ID215	ext-est-not-vrt	6.7	Muscle	27-21-2-C8-PU
ID216	ext-est-not-vrt	6.7	Heart	67-1-1-C8-PU
ID217	ext-est-not-vrt	6.3	Fetal kidney	58-26-3-G6-PU
ID218	ext-est-not-vrt	6.2	Fetal kidney	58-15-3-B12-PU
ID219	ext-est-not-vrt	6	Muscle	27-5-2-G11-PU
ID220	ext-est-not-vrt	6	Fetal kidney	58-8-1-H10-PU
ID221	ext-est-not-vrt	5.8	Fetal kidney	58-38-4-D2-PU
ID222	ext-est-not-vrt	5.6	Fetal kidney	58-53-2-E6-PU
ID223	ext-est-not-vrt	5.6	Fetal kidney	58-52-2-C7-PU
ID224	ext-est-not-vrt	5.5	Fetal kidney	58-34-2-E7-PU
ID225	ext-est-not-vrt	5.4	Fetal kidney	58-4-1-A2-PU
ID226	ext-est-not-vrt	5.2	Fetal kidney	58-11-1-D3-PU
ID227	ext-est-not-vrt	5.2	Fetal kidney	58-34-3-C9-PU
ID228	ext-est-not-vrt	5.2	Fetal kidney	58-35-4-H11-PU
ID229	ext-est-not-vrt	4.6	Fetal kidney	58-3-4-H7-PU
ID230	ext-est-not-vrt	4.5	Fetal kidney	58-25-1-F3-PU
ID231	ext-est-not-vrt	4.5	Fetal kidney	58-4-4-A8-PU
ID232	ext-est-not-vrt	4.4	Fetal kidney	58-11-1-C1-PU
ID233	ext-est-not-vrt	3.9	Muscle	27-19-2-F5-PU
ID234	ext-est-not-vrt	3.5	Dystrophic muscle	29-2-2-A2-PU
ID235	est-not-ext	14.1	Fetal kidney	58-29-2-B9-PU
ID236	est-not-ext	11.4	Dystrophic muscle	29-11-2-E4-PU
ID237	est-not-ext	11.2	Fetal kidney	58-7-2-A7-PU
ID238	est-not-ext	10.8	Muscle	27-22-3-G4-PU
ID239	est-not-ext	9.9	Fetal kidney	58-9-1-G1-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID240	est-not-ext	9.7	Dystrophic muscle	29-8-1-H5-PU
ID241	est-not-ext	9.6	Fetal kidney	58-40-1-F5-PU
ID242	est-not-ext	9.5	Fetal kidney	58-6-4-G2-PU
ID243	est-not-ext	9.2	Fetal kidney	58-25-2-E7-PU
ID244	est-not-ext	8.9	Fetal kidney	58-48-1-A11-PU
ID245	est-not-ext	8.8	Fetal kidney	58-35-2-B6-PU
ID246	est-not-ext	8.5	Kidney	21-7-4-C7-PU
ID247	est-not-ext	8.4	Fetal kidney	58-45-1-E6-PU
ID248	est-not-ext	8.1	Fetal kidney	58-39-1-A12-PU
ID249	est-not-ext	8	Fetal kidney	58-46-1-C7-PU
ID250	est-not-ext	7.9	Dystrophic muscle	29-12-3-E10-PU
ID251	est-not-ext	7.9	Fetal kidney	58-17-2-D9-PU
ID252	est-not-ext	7.9	Fetal kidney	58-52-3-B7-PU
ID253	est-not-ext	7.6	Fetal kidney	58-24-3-E7-PU
ID254	est-not-ext	7.6	Heart	25-8-4-B12-PU
ID255	est-not-ext	7.6	Dystrophic muscle	29-4-4-D12-PU
ID256	est-not-ext	7.4	Muscle	27-1-2-B3-PU
ID257	est-not-ext	7.3	Fetal kidney	58-48-1-G3-PU
ID258	est-not-ext	7.3	Dystrophic muscle	29-2-3-F8-PU
ID259	est-not-ext	7.2	Fetal kidney	58-19-3-B3-PU
ID260	est-not-ext	7	Fetal kidney	58-14-2-C4-PU
ID261	est-not-ext	6.7	Fetal kidney	58-16-3-B6-PU
ID262	est-not-ext	6.6	Fetal kidney	58-9-4-F6-PU
ID263	est-not-ext	6.4	Fetal kidney	58-1-1-E3-PU
ID264	est-not-ext	6.4	Fetal kidney	58-33-3-B4-PU
ID265	est-not-ext	6.3	Dystrophic muscle	29-12-1-H1-PU
ID266	est-not-ext	6.3	Muscle	27-9-3-A5-PU
ID267	est-not-ext	6.2	Muscle	27-17-4-C12-PU
ID268	est-not-ext	6.2	Fetal kidney	58-33-1-F1-PU
ID269	est-not-ext	5.9	Fetal kidney	58-48-4-H2-PU
ID270	est-not-ext	5.9	Fetal kidney	58-42-1-A6-PU
ID271	est-not-ext	5.7	Fetal kidney	58-33-4-E1-PU
ID272	est-not-ext	5.7	Fetal kidney	58-26-2-E12-PU
ID273	est-not-ext	5.6	Fetal kidney	58-26-1-E12-PU
ID274	est-not-ext	5.5	Fetal kidney	58-54-1-D11-PU
ID275	est-not-ext	5.5	Muscle	27-9-2-F9-PU
ID276	est-not-ext	5.4	Fetal kidney	58-30-2-H10-PU
ID277	est-not-ext	5.3	Fetal kidney	58-29-1-H1-PU
ID278	est-not-ext	5.3	Kidney	21-1-4-F2-PU
ID279	est-not-ext	5.1	Fetal kidney	58-42-4-H7-PU
ID280	est-not-ext	5	Fetal kidney	58-34-3-H10-PU
ID281	est-not-ext	5	Kidney	21-7-3-B4-PU
ID282	est-not-ext	4.9	Fetal kidney	58-4-2-D12-PU
ID283	est-not-ext	4.8	Fetal kidney	58-31-2-C10-PU
ID284	est-not-ext	4.7	Fetal kidney	58-37-3-C10-PU
ID285	est-not-ext	4.7	Fetal kidney	58-1-1-D11-PU
ID286	est-not-ext	4.6	Fetal kidney	58-52-1-A11-PU
ID287	est-not-ext	4.3	Fetal kidney	58-4-3-E10-PU
ID288	est-not-ext	4.3	Heart	67-6-4-F2-PU
ID289	est-not-ext	4.2	Fetal kidney	58-49-3-G10-PU
ID290	est-not-ext	4.1	Dystrophic muscle	29-10-3-B11-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID291	est-not-ext	4.1	Heart	25-5-4-A7-PU
ID292	est-not-ext	4.1	Fetal kidney	58-33-2-C6-PU
ID293	est-not-ext	4	Heart	25-7-3-D4-PU
ID294	est-not-ext	3.9	Heart	67-1-3-B11-PU
ID295	est-not-ext	3.9	Fetal kidney	58-23-1-G5-PU
ID296	est-not-ext	3.7	Fetal kidney	58-6-1-B6-PU
ID297	est-not-ext	3.7	Dystrophic muscle	29-6-2-H8-PU
ID298	est-not-ext	3.7	Fetal kidney	58-43-4-B8-PU
ID299	est-not-ext	3.6	Muscle	27-3-4-G9-PU
ID300	est-not-ext	3.6	Fetal kidney	58-38-1-F10-PU
ID301	est-not-ext	3.5	Heart	67-6-4-E7-PU
ID302	est-not-ext	3.5	Fetal kidney	58-54-1-E6-PU
ID303	est-not-ext	3.5	Heart	67-4-4-G7-PU
ID304	est-not-ext	3.5	Fetal kidney	58-23-4-F4-PU
ID305	ext-vrt-not-genomic	10.5	Fetal kidney	58-42-3-A12-PU

TABLE III

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID38	MMWRPSVLLLLLLLRHGAQG
ID39	MERPLCSHLCSCAMLALLSPLSLA
ID40	MIHLGHILFLLLPVAAA
ID41	MAVKLGTLALLALGLAQPASA
ID42	METLGALLVLEFLLSPVEA
ID43	MLLPLLLSSLLGGSQA
ID44	MLWLLFFLVTAIHA
ID45	MAGSPSRAAGRRLQLPLLCLFLQGATA
ID46	MKWPWTCLAILCPGPVLSPPCSGPXLALALLVLPLLWP
ID47	MPSWIGAVILPLLGLLLSLPAGA
ID48	MLLHWVRSQXXSDXKLWLSLLVPSCICA
ID49	MKYLRHRRPNATLILAGFTLLLFSLVSPPTC
ID50	MPGPRVWGKYLWRSPHSGCPGAMWWLLWGVLQA
ID51	MCGPAMFPAAGPPWPRVRVQVLWALLAVLLASWRLWA
ID52	MHRRKLPLTNKRQLQKXLSKFISDELFRNLFSLRTLRLMILSLLLSTALNILA
ID53	MKLWVSALLMAWFGVLS
ID54	MQLPLALCLVCLLVHTAFR
ID55	MLCIHXXRIQDSFIALKILLCSVAVXLSPS
ID56	MGGFFPTEVREVCANQGAHNRDRLPFLSLFWPWAPG
ID57	MKLFYNQLVSETKHDFAHLLWLLLFSCWM
ID58	MPSESPLLFFHILFHSCFS
ID59	MSSMWSEYTIGGVKIYFPYKAYPSQLAMMNSILRGLNSKQHCLLESPTGSGKSLALLCSA LAWQQSL
ID60	MALFLELFLNSYSLLFVRFLGFVSCLQS
ID61	MNEDEKEMKEILMAGSSLSAGVSG
ID62	MGSFLLGGIPLIXLXSLCLC
ID63	MLQVATTNYLELAREVKPVCLLCGSCAWS
ID64	MFCLAPFFLALCFPKSTS
ID65	MSESRFQPQNQGSLQLPLQCLCCISPPVFC
ID66	MPKHCHSFITSSCLLGLLHLSSQ
ID67	MCLLFXFIXFPFLFFFSFS
ID68	MASERXPNRXPCLLVASGXAEVSA
ID69	MFPDYKLGGSYLLAFQLVFLRATSG
ID70	MRRISLTSSPVRLLLXLXLLIALE
ID71	MTFLLLLFXNAGRS
ID72	MRTVVLTMKASVIEMFLVLLVTGVHS
ID73	MSSPLLVEQSSTKSPKSWWSFLAFSCISLLFIFFSIANS
ID74	MYLFCFLFSVSKTIPLLLFFHLSFL
ID75	MIVCLLILKFLSPAET
ID76	MDKSXSSHWSLCFLFLHTHT
ID77	MFFIFINGFTLLLMTLAMKPRHPIFDLLLLLXXSNQ
ID78	MCPSLEEAPSVKGTLPSCGQQQPFPGASNIPLLGRSRKVARGAPVLWPFLTWINPALS
ID79	MLQDLSALWFCHPCCL
ID80	MMDLRPLLSLAAYLSGPHQ
ID81	MEMPPCLLPGLPLVRTSFS
ID82	MTVELWLRLRGKGLAMLVTRGVXG
ID83	MSIEDFVNRSILLILLCSSPPDRV
ID84	MRIHYLLFALLFLFLVPVPG
ID85	MCLLTALVTQVIS

SEQ. ID NO.	SIGNAL PEPTIDE
ID86	MMGNPGLALVAGTPPSRS
ID87	MNHLMPLTVLHSVLEMLRTPRTPPWPCVSLWAPRXFA
ID88	MGHVVFQDIKNSLLXLRASQLSEG
ID89	MAGGRDYSQLFGRGPGRLSRARASVVRWSPRATACAPPSPDLKRQELVSRIECGCRG PVGATADFFLSLLXSVSETPG
ID90	MFWXGSLWCFHSFISFSLS
ID91	MAWPNVFQXGSLLSQFXXHVVVFLLTFFSYSLHA
ID92	MILRNLWILAVGLSLPSSS
ID93	MLTVNDVRFYRNVRSNHFFVRLCGLLHLWLKVS
ID94	MNLKPGLPCNLFNLCLAXPFS
ID95	MMQGEAHPASLIDRTIKMRKETEARVVLAWGLLNVSMA
ID96	MMNQTHPXXLLLAHITQS
ID97	MGLPERRGLVLLSLAEILF
ID98	MWGLEEDRSYQGLRPLCWALLYNCFSSS
ID99	MLCRDGSACVPRSRLPLPAAVRAHGPMADXXDSARGCVVFEDVFVYFSREEWELL DDAQRLLYHDVMLENFALLASLGIAFSRS
ID100	MLITRLQSGIDFAIQDESTDIGSCTLLVYVRYAWQDDFLEDFLCFLNLTSHLSG
ID101	MESPLQHCILNSNSVACSFVAGAGFLAFLSCLAFLVLD
ID102	MSNKYIKPSMSPGNTDHLFLLFPRSCSS
ID103	MVELKQLGPRSFFFFLFLPPXPP
ID104	MPYVTIPYIIVYSLIPALFFFLHC
ID105	MPPLAAVMGSLPLLLCMDLPHSVLS
ID106	MLQIPERREFLFLGFPSNSWP
ID107	MFFVHFLITLFCCCVVVG
ID108	MACFGEKRHAKSCLLHLRCLQLYWA
ID109	MVDRDENILLKQIYSPLSLALQSSCCLC
ID110	MKVKPPFVSVSLCVCDCVRG
ID111	MISSCGVKYLFSHASLFFMVGSTGSLILLTSCFYTLVSS
ID112	MGGGIAESFLCNFLVSLSL
ID113	MDALERGLRNEQALVITYAGLAYFLCCQGVIFG
ID114	MEYLFQQPGHSRGEARAAAASLETLSLWFLPLPTHVYT
ID115	MVSSMLITLSFIFA
ID116	MPLFTMNLVSALASSAXG
ID117	MICKHYCIKKNLDYLNRMVYSAQLKLILLHCSIRVFF
ID118	MKIPVWHKTCFLKSESPDNLSVSLPCRPSQVPSQGQGSFLLQLIHEDKA
ID119	MGAAVFFGCTFVAFXPAFA
ID120	MVGGLDPPGRRRFQKGFWRNLWSSCWLA PLADG
ID121	MSKMPVFASLLVVSIFYQISG
ID122	MXVTQLLPFSSPDSA
ID123	MGKAWQEMRVEWGADKGNVRSSFHFLPWALGAMA
ID124	MKVMRKRKKKDQCLPGICRSLKRRKSPRSPGMKVIRLSQFLLKCWP
ID125	MTFSFFCFPGFK?LLFHYFLXSFISIXTLLWGLNC
ID126	MAGGMKVAVSPA VGPWPWGSGVGGGGTVRLLLLILSGCLVYG
ID127	MVEMTG VWQCQAEAVKGLPPLLSCSCPPPLG
ID128	MQITPGSAAGLLPLLLGNAPG
ID129	MILSTWLLTLQNSVFT
ID130	MAFHSYWGKSLQSFKTFMRVCIVLALCHTSRP
ID131	MKLRFTLLPLVLHSQS
ID132	MMILGFAFCPGHFRFNFIPLVITYSFVLS
ID133	MNRVPADSPNMCLICLLSYIALGAIHA
ID134	MDLFLNLPLVIGTIP

SEQ. ID NO.	SIGNAL PEPTIDE
ID135	MXKNHRNKKSIHFPLCTIPSMXKSCITLPLQRTWDXXPSFVHWXQARLQSPPXSHLVXLS VIRSTLVLSQCLC
ID136	MSFIALVYSSLSFQ
ID137	MVFDTLKSRIVLFLNSXFPIIC
ID138	MLEMENTWLRLCDECSRWGMASAWGRGGKLLGAQVALHPRNCSKAKIFLFSILLMSLRT
ID139	MDDLMLFFLGALCRESG
ID140	MVLGALNLPSEQELPTLLLLPVGAPG
ID141	MLVSKIQTFFVSFLSIPVLG
ID142	MCNPVAHTFRGVHEHHAMLLSTGLNILGTQA
ID143	MQCWILLWEACTGRCQA
ID144	MTGYPWANSITTVLCILGCHGNLCC
ID145	MVSCDVXSYYIIFTALFLXLHSA
ID146	MKSFDKKLFAIFLMCLKSIG
ID147	MFGAGDEDDTDFLSPSGGARLASLFGLDQXAXG
ID148	MVLTLGESWPVLVGRRLSLSAADGXDX
ID149	MVIELTSVFQAMIWSQG
ID150	MESTLGAGIVIAEALQNQLAWLENVWLWXXLXXXIPXILFLFYFPAAYYA
ID151	MIIVSELGTPGVLVGVFLSTFLYC
ID152	MNWNVRGTRGFLLCPLVCGLRR
ID153	MLRCGGRGLLLGLAVAAAA
ID154	MILLMIVFSIFLL
ID155	MSLLFIFRSILISC
ID156	MPLISKVLIQLSQAFWA
ID157	MDTSSVGLELTDQTPVLLGSTAMATSLT
ID158	MDTGESFSPHTSCRGHWRILLTHVPPWILE
ID159	MPYLDPYITQPIQIERKLVLLSVLKEPVSR
ID160	MDTSSVGLELTDQTPVLLGSTAMATSLT
ID161	MHVLFNIVTTNXXNHFGLLDFVVQCCDS
ID162	MPPQSCCSKTAYWLSFMSWAQS
ID163	MSCVFFHFLOQGLG
ID164	MSISLSSLILLPIWINMAQI
ID165	MTALNLVAPFSDGDSGSVSLASFCAVVLSPVFQ
ID166	MWSRPVQVLGLLATCQH
ID167	MRYRLRIQITTSLNQILLFLLISC
ID168	MPFFSNQPTQVSLLFFCCSPLYSP
ID169	MRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVSNA
ID170	MVSLGYLIFVLYLWLCFMQISEEKLIEHTGTALTSSPLCQL
ID171	MSLTSRXXIMXTIKIQNISITKVLCCLLIATPTFF
ID172	MXAEAAGVVSTSVAAAVA
ID173	MWIMSSCLALTYTNS
ID174	MPRGVYNSNALVLVTRGSSS
ID175	MIEPCEKMKHYDMNWFLCMYECFFHLLLETEFLPCVHPFSVIA
ID176	MAMWNRPCQXLQQPLVAEPTAEGEPHLP TGRELTEANRFAYAALCGISLSQXFP
ID177	MEQVCLLVSYAVDSAAG
ID178	MRKISHCLHCWPESGATLRCWASTPVSG
ID179	MCINDHIIKLLHPCGSITLTSS
ID180	MRCRVALQCGLTIPALX
ID181	MTVRYGKFLSLLKDGAEENDLTWVLKHCFERFLKQQQTSIKSSLLCLQGNYAGHDWVFVSSLF MIMLGDKETTFQLHQFSRLLTSAFLWLPRLHI
ID182	MAFDVSCFFWVVLFSAGCKV
ID183	MLTRLVLSAHLSTTSPPWTHA

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID184	MRYFQGSPSPYSEIEIELCDHVYSFQGLCVNLLLGFEFVIS
ID185	MXXKRTHXXXSVFNGLVYAAGGRNAEGSLASLECYVPSTNQ
ID186	MFLKVQSQSFYXPYRDCLNFHKSTYLLFFHLLLNDFFT
ID187	MQPLKIIFYLSVSIWILIIYTFQCNS
ID188	MMRTTARVA ACTAAAPLQA
ID189	MEAATTLHPGPRPALPLGARARWASSCLHPSARS
ID190	MQGVRGPVSFSWSTTMLCPVIFFPSNCWK
ID191	MXXFSFXLLFXFXFFRQ
ID192	MLLLSEALSESVRLLFRFSVIMA
ID193	MALISLPCTTAFPLLSS
ID194	MSEEEAAQIPRSSVWEQDQONVVQRVVALPLVRATCT
ID195	MAAAAAAGAASGLPGPVAQGLKEALVDTLTGILSPVQEVRAAAEEQIKVLEVTEEFGVHL AELTVDPQGALA
ID196	MNSGGGFGGLGLGFLTPTSVIQVTNLSSAVTSEQMRTLFSFLGEIEELRLYPDNAPLAF SSXVCYVKFRDPSSVGVAQHLLTNTVFIDRXLXSCSLCRRLVSRFXXXLYNFCPVCYC
ID197	MIEMLIFLDCVLS
ID198	MHPFLAAHGPAFHKGKYSTINIVDIYPMCHILGLKPHPNNGTFGHKCLLVDQWCINL PEAIAIVIGSLLVLTMLTC
ID199	MIWPMSASVATLWS
ID200	MGIDIFYPSHIPDFHPIHLFIYLVFVECLLC
ID201	MKELNQKLTNKNKIEDLEQEIQKQKQETLQEEITSLQSSVQEEKNXKIKQLLVKT KKELADSKQAETDHLILQASLKGELEA
ID202	MGNTLKEMQDVQGALQCYTRAJQINPAFADAHSNLASIHKDSGNIPEAIASYRTALKLKP DFPDAYCNLAHCLQIVCDWTDYDERMKKLVSIVADQLEKNRLLLCILIVCYT
ID203	MLILADTRRVQGGTLGLIPAVLNRVHVAYAPSIPSLFC
ID204	MLVGIYFCVFLFPLISNTSS
ID205	MFLAPSLITKLLTGSESPDGNPPALGRPLLLQGACPLIFL
ID206	MDPSASKSCLFYLQKVSG
ID207	MSLTASGPRAAWEERVGGLHTWGANIPTAPDSQRWLCLQAYLASFS
ID208	MKYQMVSGSAQLASPLPGATP
ID209	MNGTFPGTYVYLVAYGDLRIFGCFWGLMYXWLLLG
ID210	MGPSTPLLILFLLSWGPLQG
ID211	MKFISTSLLLMLLVSSLSPVQG
ID212	MNYQYGFNMVMSHPHAVNEIALSLNNKNPRTKALVLELLAAVCLVRG
ID213	MAQSIHMYAARVQWGLVMCFLSYFGTFA
ID214	MGSYSHSLHLFHLIRPXQG
ID215	MARCFSLVLLTTSIWT
ID216	MAMRYNRLTVLAGAMLALGLMTCLSVLFGYATS
ID217	MPQQPVEQGSPLLRLQLLPLPPFSFP
ID218	MPSRSPFTWSHLCWRAGRCPRWRACLSSSSVRMCSPAAPSRFGALGXSARRWPRRDA DTWCAPQGVMRASLLPMLLGSA
ID219	MSHTEVKLKIPFGNKLLDAVCLVPNKSLTYGILTHGASG
ID220	MELGSCLEGGREAAEEEGEPEVKRRLLCXEFXSVASDA
ID221	MGRTYIVEETVGQYLSNINLQGKAFVSGLLIGQCSS
ID222	MGSRKCGGCLSCLLIPLALWS
ID223	MGSRKCGGCLSCLLIPLALWS
ID224	MWWFQQLSFLPSALVIWTS
ID225	MFNASTFTDWSSSIFVFTFKSKKSAGLPLIFSLWCSGVLL
ID226	MKMASSLAFLLLNFHVSLLLVLQLLTPCSA
ID227	MHILQLLTTVDDGIQAIVHCPDTGKDIWNLLFDLVCHFCQS
ID228	MSDQIKFIMDSL NKEPFRKNYNLITFXSLEPMQLLQVLSDVLA

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID229	MATSSQXRQLSDYGPPLSGYTQGTGNSQXPQSKYAELLAILXELGKEIRPMYAGSKSAM ERLKRGIHAXGLVRECLA
ID230	MRLLGAAAVALGRG
ID231	MAQRLLRRFLASVIS
ID232	MFRLNSLSALAELAVG
ID233	MSGSNKSKENSHNKARTSPYPGSKVERSQVPNEKVGWLVEWQDYKPVEYTA VSVLA GPRWA
ID234	MRTTLMFSLTAQWXTS
ID235	MSDLLLLGLIGGLTLLLLTLLAFA
ID236	MEGTEMGARPGGHPXKWSFLWSLALWLPLALS
ID237	MXFLRKVXSILSLQVLLTTVTSTVFLYFESVRTFVXESPALILLFALGSLGLIFA
ID238	MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQG
ID239	MSSWMYLGYPVTSNTTCLKLISSEFPQILPFLFPFPVNA
ID240	MAPGVIIIQLCLLLPSCSL
ID241	MRHGFQQQFSLTAFSXXXXIFTLXXLSQLLSSAAPKHTAAPTALPCLQGQQNLNLSLGT SELSCVLASSCLSTKTDPSGLSLSLGASAPVQC
ID242	MFQNIQKCLNVFVRGYHVFIYNLNAVILIFLSFLPFINS
ID243	MSLSQRGFPVLALFLSGSLA
ID244	MAARWRFWCVSVTMVVALLIVCDVPSASA
ID245	MFAPAVMRAFRKNKTLGYGVPMLLLVGGSGF
ID246	MELPSGPGPERLFDSHRLPGDCFLLLVLLYAPVGFC
ID247	MAQSQGWVXRYXKAFCKGFFVAVPVAVTFLDRVACVARVEGASMQPSLNPGGXSXSS DVVXXNHWKVRNFEVHRGDIVSLVLLTVTPSXRQ
ID248	MSSAAADHWAWLLVLSFVFGCNV
ID249	MNLFKTNHVFFLLLAHIIA
ID250	MPALLPVASRLLLLPRVLLTMASG
ID251	MIGSLAGSGGAGGPSSTVTWCALFSNHVAATQASLLLSFVWMPALLPVASRLLLLPRVL LTMASG
ID252	MPALLPVASRLLLLPRVLLTMASG
ID253	MEASWGSFNAERGWYVSQQPEEAEAEELSPLLSNELHRQSPGVSFGLSVFNLMAIMG SGILGLAYVMANTGVFGFSFLLLTVALLASYS
ID254	MPSSFFLLLRFFLRIDG
ID255	MKRTHLFIVGIYFLSSCRA
ID256	MGDKIWLFPVLLLAALPPVLLP
ID257	MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTWGLG
ID258	MGAWGRGWPEERQGHLLLLLLPAPTLK
ID259	MGQCGITSSKTVLVFLNLIFWGAAGILCYVGAYVFITYDDYDHFFEDVYTLIPAVVIIAV RALLFIIGLIGCCAT
ID260	MPXAFSVSSFPVSIPAVLTQTDWTEPWLMGLATFHALCVLLTCLSSRSYRLQIGHFLCLV ILVYC
ID261	MLLLSLFFPLRISL
ID262	METGERARLELVQLLRRR
ID263	MCGXXFSLPCLRLFLVVTCTYXLLLLHKEILGCSSVCQLCTG
ID264	MNPVTESPSCLFSPSESALASQLALSASCDQRAPFSLAGVXSXXPRLASRQVAPPFGSR ACCFLSAFSPTLT
ID265	MSRSSKVVLGLSVLLTAATVA
ID266	MGIQTSPVLLASLGVGLVTLLGLAVG
ID267	MYPYLLIXPPIPSQLKQCPPTLSDPFLPLALRSLDVLLSSAXLVXXS
ID268	MEQKHXELEQLKLXTKENKILLXTFQTWCLR
ID269	MMTAPVLAAQTLKFLTLLQKSNA
ID270	MDSAACAAAATPVPALALAXAPDLAQA

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID271	MASLGLQLVGYILGLLGLLGTLVA
ID272	MASLGLQLVGYILGLLGLLGTLVA
ID273	MLCSLLLCECLLLVAGYA
ID274	MASRLCGGALWYVCPSPGAWM
ID275	MTSALTQGLERIPDQLGYLVLSEGAVLA
ID276	MASPSRRLQTKPVITCFKSVLLIXTXIXWITGVILLAVGIWG
ID277	MADAASQVLLGSGLTILSQP
ID278	MSRNLRTALIFGGFISLIGA
ID279	MPHGLWCFHLVVLSTLYS
ID280	MSLVAVFLSCGLIS
ID281	MMKRAAAAAVGGALAVGAVPVVLS
ID282	MAVIVDKPWFYDMKKVWEGYPIQSTIPSQYWYYMIELSFYWSLLFSIASDVKRKDFKEQI IHHVATIILISFSWFANYTRA
ID283	MIISLFIYFLTCSNT
ID284	MAAELVEAKNMVMSFRVSDLQMLLGFVGRSKS
ID285	MTGLSMXGGGSXXGDVXPXYGKXGPLRXLPEPSGPLPPSSGLSQPVHALCPLSPLVTT
ID286	MQMYSRQLASXEWLTIQGGLLGXGLXXXSLT
ID287	MASLEVSRSPRRSRRELEVSRPNKYSVLLPTYNERENPLIVWLLVKSFSSES
ID288	MDKDSQGLLDSSLMASGTAS
ID289	MGLLTFGYIEXXKTEHNPDHHSCLAVSWEAAGCHG
ID290	MGLYAAVAGVLAGVES
ID291	MGLYAAAAGVLAGVESRQSGIKGLVYSSNFQNVKQLYALVCETQRYSAVLDAVIASA GLLRA
ID292	MGAQHTALLNTEVRWLSRGKVLVRLFELRRELLVFMDSAFRLSDCLTNSSWLLRLAYLA DIFT
ID293	MSLRNLWRDYKVLVVMVPLVGLIHL
ID294	MVLRSLVEYSQDVLAPVSEEHLDPVSLIGFSDPAELGKLLQLVLGCAIS
ID295	MIHGFCLAPTTSA
ID296	MXCPRTWCLACVEASPG
ID297	MADVEDGEETCALASHSGSSG
ID298	MFKVAAPPMLIXXIIMFLIIVCGSP
ID299	MDFWDPAVFXMCLWSLRNLFS
ID300	MSPAGKHNSKFTFFVALDGSVPLLSLSHSIGI
ID301	MHWALVCVGLHTEGPWG
ID302	MFGAAARSADLVLEKNLQAAHGYAQEDRERMHRXIVSLXQNLLNFMIGSILDLWQCF LWFYIGSSLNGTRG
ID303	MAARWRFWCVSVTMVVALLIVCDVPSA
ID304	MVVLLQLQPSMIQEVWT
ID305	MLHLHXSCLCFRSWLPAMLA VLLSLAPSASS

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0.121	0.036	0.467	0.664
4	0.096	0.06	0.519	0.708
4.5	0.078	0.079	0.565	0.745
5	0.062	0.098	0.615	0.782
5.5	0.05	0.127	0.659	0.813
6	0.04	0.163	0.694	0.836
6.5	0.033	0.202	0.725	0.855
7	0.025	0.248	0.763	0.878
7.5	0.021	0.304	0.78	0.889
8	0.015	0.368	0.816	0.909
8.5	0.012	0.418	0.836	0.92
9	0.009	0.512	0.856	0.93
9.5	0.007	0.581	0.863	0.934
10	0.006	0.679	0.835	0.919

TABLE IV

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Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3.5	2674	947	599	23	150
4	2278	784	499	23	126
4.5	1943	647	425	22	112
5	1657	523	353	21	96
5.5	1417	419	307	19	80
6	1190	340	238	18	68
6.5	1035	280	186	18	60
7	893	219	161	15	48
7.5	753	173	132	12	36
8	636	133	101	11	29
8.5	543	104	83	8	26
9	456	81	63	6	24
9.5	364	57	48	6	18
10	303	47	35	6	15

TABLE V

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

TABLE VI

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (648 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	9	TGTCAGTTG
MYOD_Q8	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.968	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-384	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHA47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETA47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETA1F2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-128	+	0.983	13	AGTTGGGAATTCC
IK2_01	-128	+	0.985	12	AGTTGGGAATTCC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRY_02	-41	-	0.951	12	TAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P15B4 (861bp) :

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q8	-748	-	0.958	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTGGAA
STAT_01	-673	-	0.951	9	TTCCAGGAA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTC
MZF1_01	-424	+	0.968	8	AGAGGGGA
SRY_02	-398	-	0.955	12	GAAAACAAAACA
MZF1_01	-218	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	18	-	0.986	8	AGAGGGGA

Promoter sequence P29B8 (656 bp) :

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.983	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGGTCTC

TABLE VII

CLAIMS

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-305 or comprising a sequence complementary thereto.
- 5 2. The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.
3. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.
4. A purified or isolated nucleic acid comprising at least 15 consecutive bases of
10 one of the sequences of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.
5. The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.
6. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-305 or one of the
15 sequences complementary to the sequences of SEQ ID NOs: 38-305.
7. The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.
8. A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-305.
- 20 9. A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-305 or having a sequence complementary thereto.
10. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-305 which encode a signal peptide.
11. A purified or isolated polypeptides comprising a signal peptide encoded by
25 one of the sequences of SEQ ID NOs: 38-305.
12. A vector encoding a fusion protein comprising a polypeptide and a signal peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-305 operably linked to a second nucleic acid encoding a polypeptide.
- 30 13. A method of directing the extracellular secretion of a polypeptide or the insertion of a polypeptide into the membrane comprising the steps of:

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

14. A method of importing a polypeptide into a cell comprising contacting said
5 cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-305 operably linked to said polypeptide.

15. A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-305, comprising the steps of:

obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-305;

10 contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-305 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

identifying a cDNA which hybridizes to said detectable probe; and

isolating said cDNA which hybridizes to said probe.

15 16. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

17. The cDNA of Claim 16 wherein said cDNA comprises the full protein coding
20 sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

18. A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-305, comprising the steps of:

contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

25 hybridizing said first primer to said polyA tail;

reverse transcribing said mRNA to make a first cDNA strand;

making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-305; and

30 isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

19. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 18.

5 20. The cDNA of Claim 19 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

21. The method of Claim 18, wherein the second cDNA strand is made by:
contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the
10 sequences of SEQ ID NOs 38-305 and a third primer having a sequence therein which is included within the sequence of said first primer;

performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product;

contacting said first PCR product with a second pair of primers, said second pair of
15 primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NOs 38-305, and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and

performing a second polymerase chain reaction, thereby generating a second PCR product.

20 22. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 21.

23. The cDNA of Claim 22 wherein said cDNA comprises the full protein coding
25 sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

24. The method of Claim 18 wherein the second cDNA strand is made by:
contacting said first cDNA strand with a second primer comprising at least 15
consecutive nucleotides of the sequences of SEQ ID NOs: 38-305;

hybridizing said second primer to said first strand cDNA; and

30 extending said hybridized second primer to generate said second cDNA strand.

25. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-305 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 24.

5 26. The cDNA of Claim 25, wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

27. A method of making a protein comprising one of the sequences of SEQ ID NO: 306-573, comprising the steps of:

10 obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NO: 38-305;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

15 isolating said protein.

28. An isolated protein obtainable by the method of Claim 27.

29. A method of obtaining a promoter DNA comprising the steps of:

obtaining DNAs located upstream of the nucleic acids of SEQ ID NO: 38-305 or the sequences complementary thereto;

20 screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and

isolating said DNA comprising said identified promoter.

30. The method of Claim 29, wherein said obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NO: 38-305 or sequences complementary thereto.

25 31. The method of Claim 30, wherein said screening step comprises inserting said upstream sequences into a promoter reporter vector.

32. The method of Claim 30, wherein said screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

30 33. An isolated promoter obtainable by the method of Claim 32.

34. An isolated or purified protein comprising one of the sequences of SEQ ID NO: 306-573.

35. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one of the sequences of
5 SEQ ID NOs: 38-305, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305, or a fragment thereof of at least 15 consecutive nucleotides.

36. The array of Claim 35 including therein at least two of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

10 37. The array of Claim 35 including therein at least five of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

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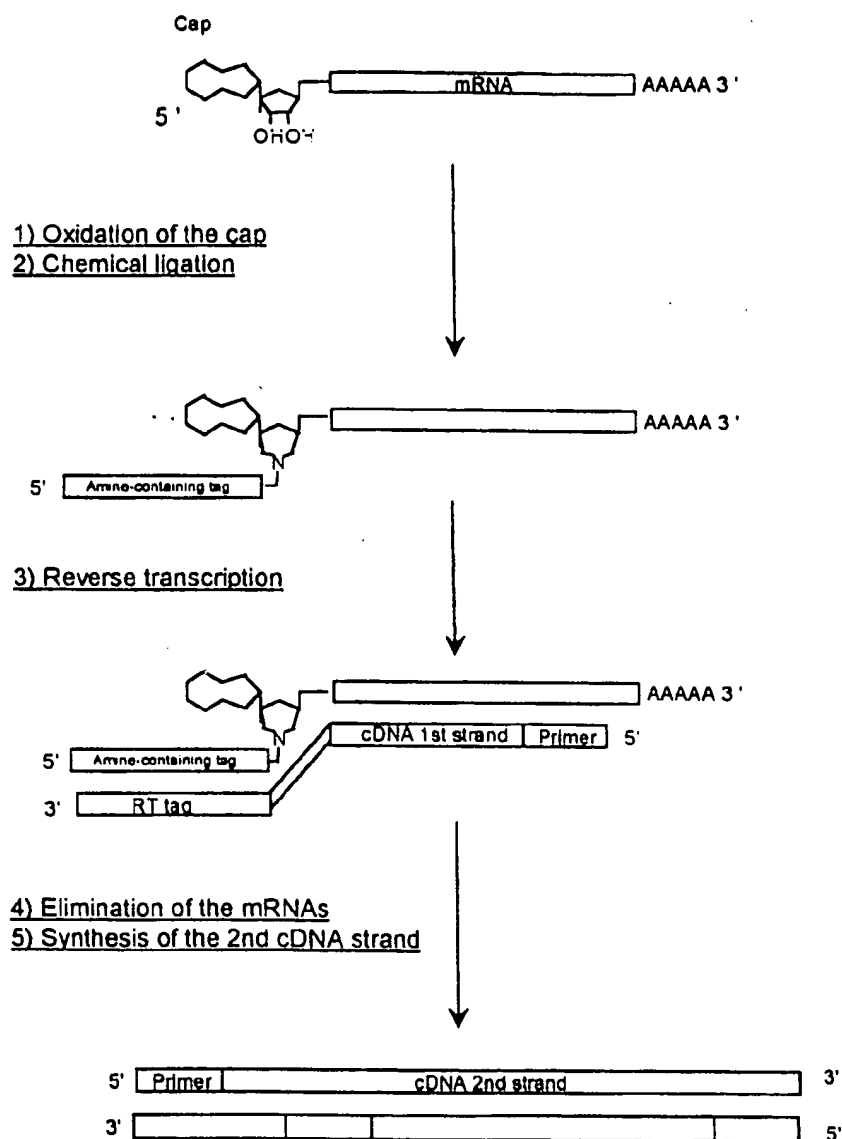


Figure 1

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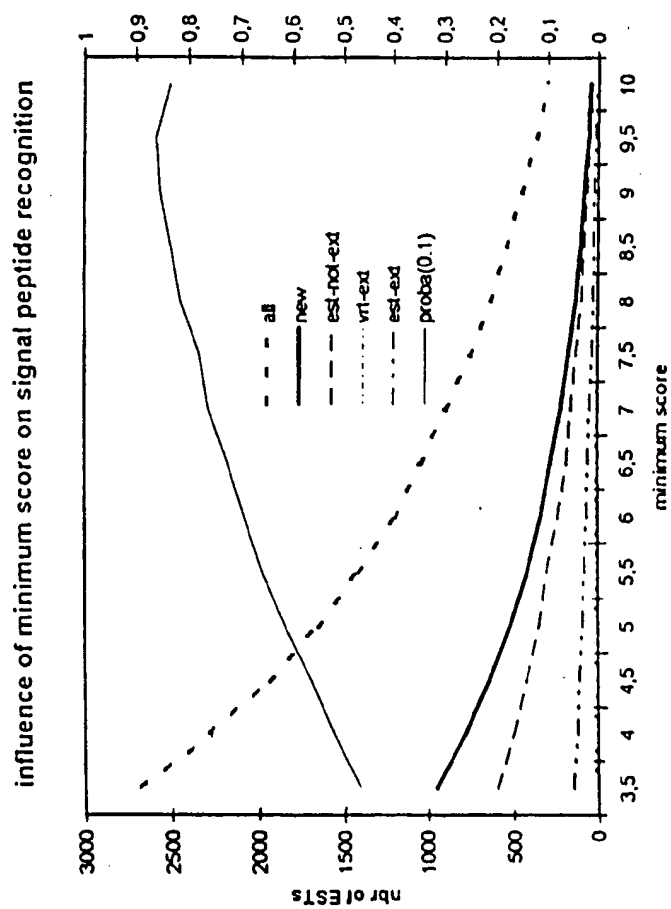


Figure 2

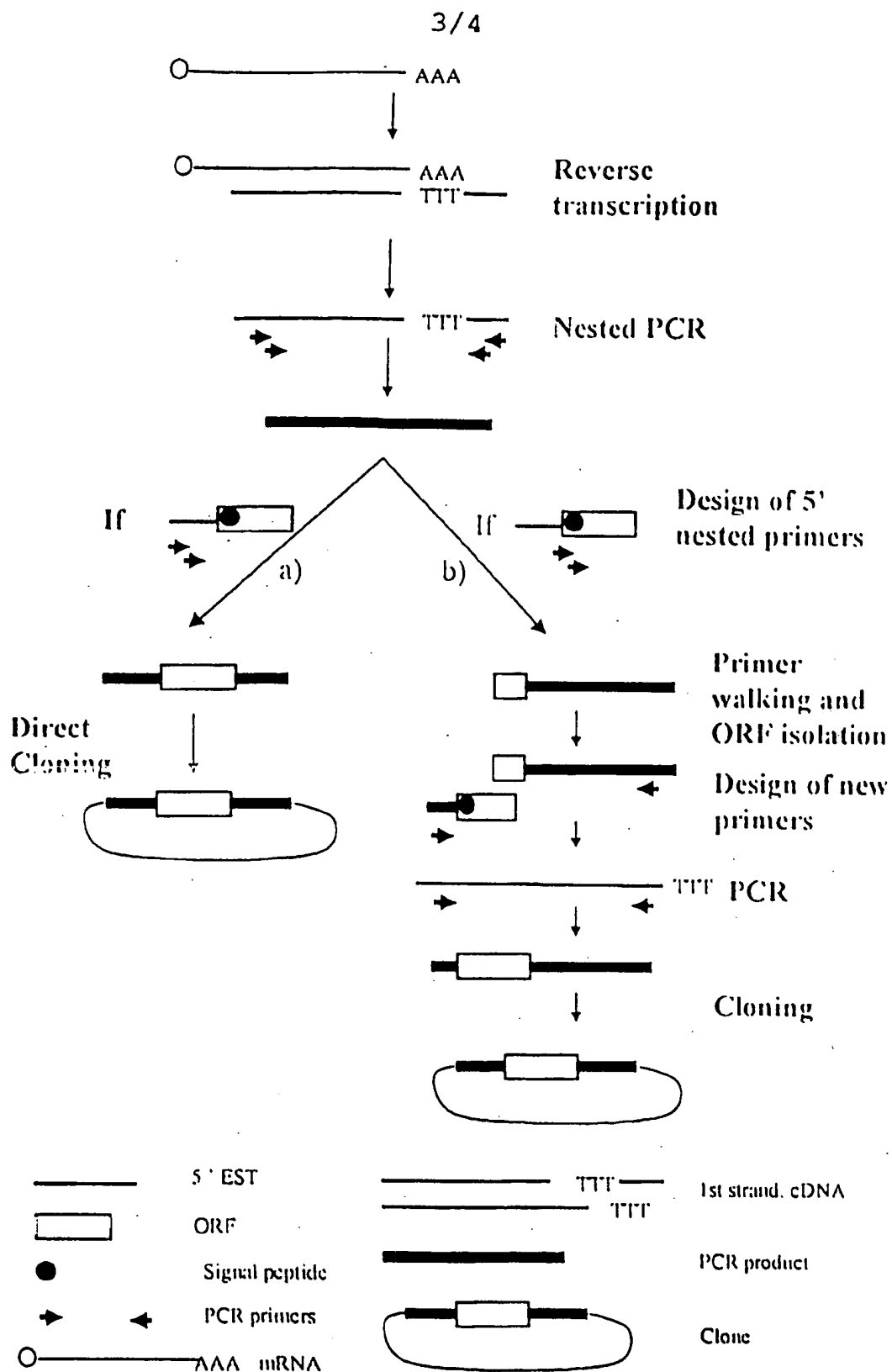
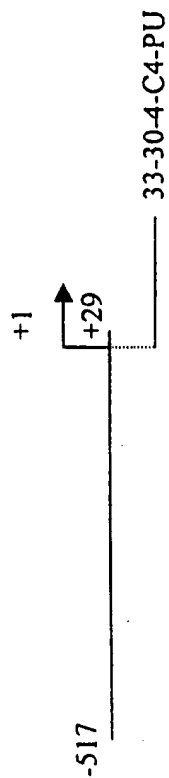
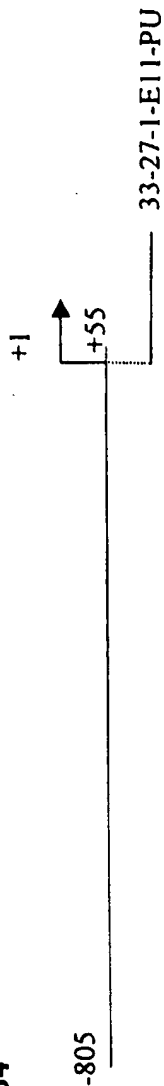


Figure 3

Promoter P13H2



Promoter P15B4



Promoter P29B6

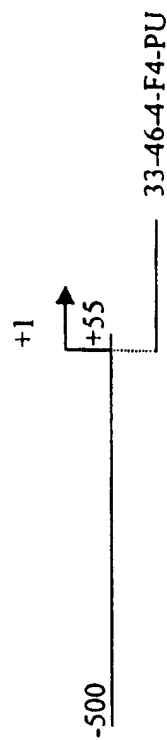


Figure 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME : GENSET SA
- (B) STREET : 24, RUE ROYALE
- (C) CITY: PARIS
- (E) COUNTRY : FRANCE
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

(iii) NUMBER OF SEQUENCES: 573

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: Cap
- (B) LOCATION: 1
- (D) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UCCACCCUA ACUCCUCCCA UCUCCAC

47

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC

46

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCAGGAGAC CATT

25

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT

25

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC

25

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGAATGG GAGACAAGCC AATTT

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AACAGCGTG AGTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA

25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG

25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CGCACGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTTT 60

TTTTTVN 67

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG 29

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG 25

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(261..376)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 166..281
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(380..486)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 54..160
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(110..145)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 403..438
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(196..229)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 315..348
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 90..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.2
 seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
AATATRARAC AGCTACAATA TTCCAGGGCC ARTCACTTGC CATTCTCAT AACAGCGTCA      60
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC      113
```

	Met	Lys	Lys	Val	Leu	Leu	Leu	Ile	
		-15						-10	
ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TCT CAA GAC CAG	161								
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln									
		-5						5	
GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR	209								
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly									
		10				15		20	
WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT	257								
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile									
		25				30		35	
CCA TTT CCA AGA TTT CCA TGG TTT AGA CGT AAN TTT CCT ATT CCA ATA	305								
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile									
		40			45			50	55
CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA	354								
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys									
		60					65		
GGAAAAGTCA CRATAAACCT GGTCACCTGA AATTGAAATT GAGCCACTTC CTTGAARAAT	414								
CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA	474								
GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA	526								

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..17
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.2
seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Lys Lys Val Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 260..464
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 153..357
 id H57434
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 118..184
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 98..164
 id H57434
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 56..113
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 35..92
 id H57434
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 454..485
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 348..379
 id H57434
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 118..545
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..428
 id N27248
 est
- (ix) FEATURE:
 (A) NAME/KEY: other

(B) LOCATION: 65..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 41..345
id H94779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..344
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 408..458
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 355..405
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 393..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 346..408
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC	60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC	120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAATCAG CGGTCTAATT AATTCCTCTG	180
GTTTGTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA	240

```

CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG      300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT      357
                                     Met Trp Trp Phe
                                     -20
CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5
GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15
GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GCT CCA RAA      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30
AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45
AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAAA      602
Lys
CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGTATT GCTTTCTACA CTGTTGAATT      662
GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTARMTA GTTCTTGACT GATAAATATG      722
GTAAGGTGGG CTTTTCCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW      782
TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA      822

```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..21
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 1                      5                      10                      15

```

Ile Trp Thr Ser Ala
20

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..296
id AA442893
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60
CCCAGCCCAA GTCAGCCTTC AGCACGCGCT TTTCTGCACA CAGATATTCC AGGCCTACCT      120
GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG      180
TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
  Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
        -35                -30                -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
        -20                -15                -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
        -5                1                5                10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCARAAGGG      384
Pro Asp Asn

TTTCTAAAAA CAAAAA AAAA A      405

```

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1..37
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1 5 10 15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
20 25 30
Ser Pro Cys Leu Thr
35

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 149..331
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 1..183
id AA397994
est
- (ix) FEATURE:
 - (A) NAME/KEY: other

(B) LOCATION: 328..485
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 179..336
 id AA397994
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(182..496)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 14..328
 id AA399680
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 196..240
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AAAAAATTGG TCCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG	60
ATTAGCCGTG GCCTAGGCCG TTTAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG	120
CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG	180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT	231
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe	
-15 -10 -5	
GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT	279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser	
1 5 10	
GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG	327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser	
15 20 25	
GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT	375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr	
30 35 40 45	
TCT TCA GCC TGAAATGAAK CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT	434
Ser Ser Ala	
TGGAAGAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAAAAA	494
AA	496

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..15
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq ILSTVTALTFFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
 1             5             10             15
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                         Met Glu Arg
                                         -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
      -10             -5             1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
  5             10             15

GTC ACC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC      201
```

Val	Ser	Ser	Trp	Thr	Glu	Cys	Pro	Pro	Thr	Trp	Cys	Ser	Pro	Leu	Asp	
20					25					30					35	
CAA	GTC	TGC	ATC	TCC	AAC	GAG	GTG	GTC	GTC	TCT	TTT	AAA	TGG	AGT	GTA	249
Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Lys	Trp	Ser	Val	
				40					45					50		
CGC	GTC	CTG	CTC	AGC	AAA	CGC	TGT	GCT	CCC	AGA	TGT	CCC	AAC	GAC	AAC	297
Arg	Val	Leu	Leu	Ser	Lys	Arg	Cys	Ala	Pro	Arg	Cys	Pro	Asn	Asp	Asn	
			55					60					65			
ATG	AAK	TTC	GAA	TGG	TCG	CCG	GCC	CCC	ATG	GTG	CAA	GGC	GTG	ATC	ACC	345
Met	Xaa	Phe	Glu	Trp	Ser	Pro	Ala	Pro	Met	Val	Gln	Gly	Val	Ile	Thr	
	70						75				80					
AGG	CGC	TGC	TGT	TCC	TGG	GCT	CTC	TGC	AAC	AGG	GCA	CTG	ACC	CCA	CAG	393
Arg	Arg	Cys	Cys	Ser	Trp	Ala	Leu	Cys	Asn	Arg	Ala	Leu	Thr	Pro	Gln	
	85					90				95						
GAG	GGG	CGC	TGG	GCC	CTG	CRA	GGG	GGG	CTC	CTG	CTC	CAG	GAC	CCT	TCG	441
Glu	Gly	Arg	Trp	Ala	Leu	Xaa	Gly	Gly	Leu	Leu	Leu	Gln	Asp	Pro	Ser	
100				105					110					115		
AGG	GGC	ARA	AAA	ACC	TGG	GTG	CGG	CCA	CAG	CTG	GGG	CTC	CCA	CTC	TGC	489
Arg	Gly	Xaa	Lys	Thr	Trp	Val	Arg	Pro	Gln	Leu	Gly	Leu	Pro	Leu	Cys	
			120					125					130			
CTT	CCC	AWT	TCC	AAC	CCC	CTC	TGC	CCA	RGG	GAA	ACC	CAG	GAA	GGA		534
Leu	Pro	Xaa	Ser	Asn	Pro	Leu	Cys	Pro	Xaa	Glu	Thr	Gln	Glu	Gly		
			135					140					145			
TAACACTGTG	GGTGCCCCCA	CCTGTGCATT	GGGACCACRA	CTTCACCCTC	TTGGARACAA											594
TAAACTCTCA	TGCCCCCAAA	AAAAAAAAAA														623

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..16
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Glu	Arg	Leu	Val	Leu	Thr	Leu	Cys	Thr	Leu	Pro	Leu	Ala	Val	Ala
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 32..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG      55
                                   Met Leu Trp Leu Leu Phe Phe Leu
                                   -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT      103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
-5                               1                               5                               10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT      151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
15                               20                               25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC      199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
30                               35                               40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC      247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
45                               50                               55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA      295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
60                               65                               70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC      343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                               80                               85                               90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC      391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
95                               100                               105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439

```

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met	
110 115 120	
GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC	487
Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys	
125 130 135	
ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TTA TCA GGG ATC TGG CAA	535
Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln	
140 145 150	
CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT	583
Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa	
155 160 165 170	
AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC	631
Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro	
175 180 185	
CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT	679
Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp	
190 195 200	
GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTCTGCT TCCTCAARAA	727
Glu Arg Leu Thr Pro Leu	
205	
ATTAAACATT TGTTTCTGTG TGAAGGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT	787
WTTTGTGTTT ACCATTCTTC TTTTGTAAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA	847
C	848

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..14
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG

25

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC

26

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..517

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 518

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 17..25
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.983
sequence TGTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(18..27)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.961
sequence CCCAACTGAC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(75..85)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.960
sequence AATAGAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 94..104
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.966
sequence AACTAAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(129..139)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name DELTAEF1_01
score 0.960
sequence GCACACCTCAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(155..165)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C
score 0.964
sequence AGATAAATCCA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 170..178
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.958
sequence CTTCA GTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 176..189
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_02
score 0.959
sequence TTGTAGATAGGACA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 180..190
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C

score 0.953
sequence AGATAGGACAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1ALPHA47_01
score 0.973
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1BETA47_01
score 0.983
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1BETA1TF2_01
score 0.978
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(287..296)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.954
sequence ACCATCTGTT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(302..314)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_04
score 0.953
sequence TCAAGATAAAGTA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 393..405
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK1_01
score 0.963
sequence AGTTGGGAATCC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 393..404
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.985
sequence AGTTGGGAATTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site

(B) LOCATION: 396..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CREL_01
score 0.962
sequence TGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 423..436
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_02
score 0.950
sequence TCAGTGATATGGCA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(478..489)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.951
sequence TAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 486..493
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name E2F_02
score 0.957
sequence TTAGCGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(514..521)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.975
sequence TGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGAGTGCAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCATTCAA ATCTTCTATG	60
TCTTGATTTG CCTGCTAATT CTATTATTTT TGGAATAAAA TTAGTTTGAT GGTTCTATTA	120
GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTC TTCAGTTGTA	180
GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTCCAAA	240
ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG	300
ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAAGGGA AGAGGTCGTA	360
GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGTGATTAG	420
CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC AGAGGGTTAA AATTGTGTGT	480
TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCCTC AAACAGATTC CCATGAATCT	540
CTTCAT	546

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACCAGGGA CTGTGACCAT TGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCAAG AGAG

24

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..806

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 807

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(60..70)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name NFY_Q6
score 0.956
sequence GGACCAATCAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 70..77
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.962
sequence CCTGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 124..132
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.994
sequence TGACCGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(126..134)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name VMYB_02
score 0.985
sequence TCCAACGGT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 135..143
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.968
sequence TTCCTGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(135..143)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.951
sequence TTCCAGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(252..259)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.956
sequence TTGGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 357..368
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.965
sequence GAATGGGATTTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 384..391
- (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(410..421)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.955
sequence GAAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 592..599
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.960
sequence GAAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 618..627
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.981
sequence AGCATCTGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 632..642
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name DELTAEF1_01
score 0.958
sequence TCCCACCTTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(813..823)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name S8_01
score 0.992
sequence GAGGCAATTAT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(824..831)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TACTATAGGG CACGGGTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGGC ATGTCAGTAA 60
TGATTGGTCC CTGGGAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT 120
CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGGACAGGG 180

CTCAGAGGGC TAGGCACGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTGAGARG 240
 GGAGCATGCC TTCCCCAAC CCTGGCTTSC YCTTGGYAM AGGGCGKTTY TGGGMACTTR 300
 AAYTCAGGGC CCAASCAGAA SCACAGGCCC AKTCNTGGCT SMAAGCACA TAGCCTGAAT 360
 GGGATTTTCTAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGT TTTT 420
 CCAAATCAAG GTAACCTTGCT CCCTTCTGCT ACGGGCCTTG GTCTTGGCTT GTCCTCACCC 480
 AGTCGGAACCT CCCTACCACT TTCAGGAGAG TGGTTTTAGG CCCGTGGGGC TGTTCTGTTC 540
 CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600
 TGGGTTCTCG CCCAAAGAGC ATCTGCCCCAT TTCCCACCTT CCCTTCTCCC ACCAGAAGCT 660
 TGCCTGAGCT GTTTGGACAA AAATCCAAAC CCCACTTGGC TACTCTGGCC TGGCTTCAGC 720
 TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCCTCTG GAAATTCTCT 780
 TCCTGATGGT CCTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCCTC TCCCATTTTC 840
 TCTCTTGGGA GCAATGGTCA C 861

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTGGGATGGA AGGCACGGTA 20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGACCACAC AGCTAGACAA 20

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 1..500
- (ix) FEATURE:
 - (A) NAME/KEY: transcription start site
 - (B) LOCATION: 501
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 191..206
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name ARNT_01
score 0.964
sequence GGA[~]CTCACGTGCTGCT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.965
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.956
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MYCMAX_02
score 0.972
sequence CAGCACGTGAGT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 195..202
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.997
sequence TCACGTGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(195..202)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.991
sequence GCACGTGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(210..217)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.968
sequence CATGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 397..410
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ELK1_02
score 0.963
sequence CTCTCCGGAAGCCT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 400..409
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CETS1P54_01
score 0.974
sequence TCCGGAAGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1_Q4
score 0.963
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1FJ_Q2
score 0.961
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 547..555
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name PADS_C
 score 1.000
 sequence TGTGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```
CTATAGGGCA CGCKTGGTCG ACGGCCCCGGG CTGGTCTGGT CTGKTGTGGA GTCGGGTTGA   60
AGGACAGCAT TTGTKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT  120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA  180
AGGAACTGAC GGA CTCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA  240
GAGCAGTCAG ACAGTGCCTG GGATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT  300
CATTCTGTGC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG  360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC  420
CGTGTCTTCT GCCTGCTCCC GCTCACATCC CAACTTGTG TTCAGTCACT GAGTTACAGA  480
TTTTCCTCC TCAATTTCTC TTGTCTTAGT CCCATCTCT GTTCCCCTGG CCAGTTTGTC   540
TAGCTGTGTG GTCTC                                     555
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 63..122
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 15.8
 seq LLLLLLLLRHGAQG/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
AACATTTGCG GGAACRSAGA GCGGANSNG NGACAGCGGA GGAVSTGGAT AACAGGGGAC   60
CG ATG ATG TGG CGA CCA TCA GTT CTG CTG CTT CTG TTG CTA CTG AGG   107
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg
-20 -15 -10
```


CAC GGG GCC CAG GGG AAG CCA TCC CCA GAC GCA 140
 His Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 285..359
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14
seq LAMLALLSPLSLA/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ACTAGTTAAA AGTAAGTGGG AAAAGAGTAA ACGCGCGACT CCAGCGCGCG GCTACCTACG 60
 CTTGGTGCTT GCTTTCTCCA GCCATCGGAG ACCAGAGCCG CCCCTCTGC TCGAGAAAGG 120
 GGCTCAGCGG CGGCGGAAGC GGAGGGGGAC CACCGTGGAG AGCGCGGTCC CAGCCCGGCC 180
 ACTGCGGATC CCTGNAACCA AAAAGCTCCT GCTGCTTCTG TACCCCGCCT GTCCCTCCCA 240
 GCTGCGCAGG GCCCTTCGT GGGATCATCA GCCCGAAGAC AGGG ATG GAG AGG CCT 296
 Met Glu Arg Pro
 -25
 CTG TGC TCC CAC CTC TGC AGC TGC CTG GCT ATG CTG GCC CTC CTG TCC 344
 Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu Ala Leu Leu Ser
 -20 -15 -10
 CCC CTG AGC CTG GCA CAG TAT GAC AGC TGG CCC CAD KAM CCC GAG TAC 392
 Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa Xaa Pro Glu Tyr
 -5 1 5 10
 TTC CAG CAA CCG 404
 Phe Gln Gln Pro
 15

(2) INFORMATION FOR SEQ ID NO: 40:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 67..120
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3
seq HILFLLLLPVAAA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

AACAGTTCCT CTGGACTTCT CTGGACCACA GTCCTCTGCC AGACCCCTGC CAGACCCAG      60
TCCACC ATG ATC CAT CTG GGT CAC ATC CTC TTC CTG CTT TTG CTC CCA      108
  Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro
                -15                      -10                      -5

GTG GCT GCA GCT CAG ACG ACT CCA GGA GAG AGA TCA TCA CTC CCT GCC      156
Val Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala
                1                      5                      10

TTT TAC CCT GGC ACT TCA GGC TCT TGT TCC GGA TGT GGG TCC CTC TCT      204
Phe Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser
                15                      20                      25

CTG CCG CTC CTG GCA GGC CTC GTG GCT      231
Leu Pro Leu Leu Ala Gly Leu Val Ala
                30                      35

```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 69..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.2

seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ATTTCATCAT CCTCAGTCTT TGCAAGGCGA CAGCTGTGCC AGCCGGGCTC TGGCAGGCTC   60
CTGGCAGC ATG GCA GTG AAG CTT GGG ACC CTC CTG CTG GCC CTT GCC CTG   110
      Met Ala Val Lys Leu Gly Thr Leu Leu Ala Leu Ala Leu
            -20                -15                -10

GGC CTG GCC CAG CCA GCC TCT GCC CGC CGG AAG CTG CTG GTG TTT CTG   158
Gly Leu Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu
            -5                1                5

CTG
Leu
161

```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..122
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.9
seq LVLEFLLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

AAAAAACCTG TGGACGCCGA CCCGGGACCG CCGCTGGCTG GCTGCTGGCT CACTCGACCG   60
TC ATG GAG ACC CTG GGG GCC CTT CTG GTG CTG GAG TTT CTG CTC CTC   107
      Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu
            -20                -15                -10

TCC CCG GTG GAG GCC CAG CAG GCC ACG GAG CAT CGC CTG AAG CCG TGG   155
Ser Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp
            -5                1                5                10

CTG GTG GGC CTG GCT GCG GTA GTC GGC TTC CTG TTC ATC GTC TAT TTG   203
Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu
            15                20                25

GTC TTT CTG GCC AAC CGC CTC TGG TGT TCC AAG GCC AGG GCT GAG GAC   251
Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp
            30                35                40

```

GAG GAG GAG ACC ACG TTC AGA ATG GAG TCC GGG
 Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
 45 50

284

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AACTCACAGC ACGACCAGAG AACAGGCCTG TCTCAGGCAG GCCCTGCGCC TCCTATGCGG 60
 AG ATG CTA CTG CCA CTG CTG CTG TCM TCG CTG CTG GGC GGG TCC CAG 107
 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
 -15 -10 -5
 GCT ATG GAT GGG AGA TTC TGG ATA CCA GTG CAG GAG TCA GTG ATG GTG 155
 Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val
 1 5 10 15
 CCG GAG GGC CTG TGC ATC TCT GTN KCC CTG CTC TTT CTC CTA CCC CCG 203
 Pro Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro
 20 25 30
 ACA AGA CTG GAC AGG GTC TAC CCC AGC CGG 233
 Thr Arg Leu Asp Arg Val Tyr Pro Ser Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 32..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.7
 seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT      52
                                   Met Leu Trp Leu Leu Phe Phe
                                   -10

CTG GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
      -5                      1                      5

GCT TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
      10                      15                      20                      25

TAT GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT      196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
                        30                      35                      40

TTC TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
                        45                      50                      55

GTC CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
                        60                      65                      70

ACA GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
                        75                      80                      85

GCC ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
                        90                      95                      100                      105

GAC CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA ACC      436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Thr
                        110                      115                      120

CGG                                                                439
Arg

```

(2) INFORMATION FOR SEQ ID NO: 45:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 20..100
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.7
 seq LPLLCLFLQGATA/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

AGAGATCGCA GCCCAACCC ATG GCC GGG TCT CCT AGC CGC GCC GCG GGC CGG      52
               Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg
                   -25                               -20

CGA CTG CAG CTT CCC CTG CTG TGC CTC TTC CTC CAG GGC GCC ACT GCC      100
Arg Leu Gln Leu Pro Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala
   -15                               -10                               -5

GTC CTC TTT GCT GTC TTT GTC CGC TAC AAC CAC AAA ACC GAC GCT GCC      148
Val Leu Phe Ala Val Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala
    1                               5                               10                               15

CTC TGG CAM CGG AAG CTT GGG                                          169
Leu Trp Xaa Arg Lys Leu Gly
                   20
  
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 40..156
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.6
 seq ALALLLVLP LLWP/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

ACTGCCCTGC CCTGGCCTGA CCCCAGGCCT AQTGAGTCC ATG AAA TGG CCC TGG      54
                               Met Lys Trp Pro Trp
                               -35

ACC TGC CTT GCC ATC CTC TGT CCT GGC CCT GTA TTG TCC CCA CCA TGC      102
Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val Leu Ser Pro Pro Cys
          -30                -25                -20

TCT GGT CCA RCG CTT GCC CTA GCC CTG TTG CTA GTC CTG CCA CTG CTA      150
Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu Val Leu Pro Leu Leu
          -15                -10                -5

TGG CCC TGC TCT GTT TTT GGC CAT GCC CTG TGC TAM CCT AGC CCT GCC      198
Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys Xaa Pro Ser Pro Ala
          1                5                10

CGA AGG                                                                204
Arg Arg
15 .

```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 28..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq PLLGLLLSLPAGA/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AACCGAGCTG GATTTGTATG TTGCACC ATG CCT TCT TGG ATC GGG GCT GTG ATT      54
                               Met Pro Ser Trp Ile Gly Ala Val Ile
                               -20                -15

CTT CCC CTC TTG GGG CTG CTG CTC TCC CTC CCC GCC GGG GCG GAT GTG      102
Leu Pro Leu Leu Gly Leu Leu Ser Leu Pro Ala Gly Ala Asp Val
          -10                -5                1

AAG GGT CGG AGC TGC GGA GAG GTC CGC CAG GCG TAC GGT GCC AAG GGA      150
Lys Ala Arg Ser Cys Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly
          5                10                15

```

TTC AGC CTG GCG GAC ATC CCC TAC CAG GAG ATC GCA KGG GAA CAC TTA	198
Phe Ser Leu Ala Asp Ile Pro Tyr Gln Glu Ile Ala Xaa Glu His Leu	
20 25 30	
AGA ATC TGT CCT CAG GAA TAT ACA TGC TGC ACC ACA GAA ATG GAR GAC	246
Arg Ile Cys Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp	
35 40 45 50	
AAG TTA AGC CAA CAA AGC AAA CTC GAA TTT GAA AAC CTT GTG GAA GAG	294
Lys Leu Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu	
55 60 65	
ACA AGC CAT TTT GTG CGC ACC ACT TTT GTG TCC AGG CAT AAG AAA TTT	342
Thr Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe	
70 75 80	
GAC GGT AGG	351
Asp Gly Arg	
85	

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq LWLSLLVPSCICA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ACCACTGTGC CCAGCCATTG TCTATACAGT TTGAATAACA CACTGAAAAA ACAGATCAGT	60
GCATATCTTC CACAATTAAC AATGCATTTG TTTAGAGC ATG TTG CTG CAT TGG GTG	116
Met Leu Leu His Trp Val	
-25	
CGC TCT CAG GMT GDC AGC GAC KCN AAG CTT TGG TTG AGT TTG CTA GTG	164
Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu Trp Leu Ser Leu Leu Val	
-20 -15 -10	
CCA AGT TGT TTA TGT GCC TCC CCT TGG CCC CTT CCT TCC CTG CCA CTC	212
Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro Leu Pro Ser Leu Pro Leu	
-5 1 5 10	

CTT CTT CCT CCC AGC TTG CTG AGC TTG CTG
 Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
 15 20

242

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 122..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6
seq LLLFSLLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAACTCTT TCTTCGGCTC GCGAGCTGAG AGGAGCAGGT AGAGGGGCAG AGGCGGGACT 60
 GTCGTCTGGG GGAGCCGCCC AGGAGGCTCC TCAGGCCGAC CCCAGACCCT GGCTGGCCAG 120
 G ATG AAG TAT CTC CGG CAC CGG CGG CCC AAT GCC ACC CTC ATT CTG GCC 169
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20
 ATC GGC GCT TTC ACC CTC CTC CTC TTC AGT CTG CTA GTG TCA CCA CCC 217
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5
 ACC TGC AAG GTC CAG GAG CAG CCA CCG GCG ATC CCC GAG GCC CTG GCC 265
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10
 TGG CHC ACT CCA CCT ACC CGA TGG 289
 Trp Xaa Thr Pro Pro Thr Arg Trp
 15 20

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 26..130
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq AMWWLLLWGVLQA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

GCAGGTCCCA GATGTCCAGT TCCAG ATG CCT GGA CCC AGA GTG TGG GGG AAA      52
                               Met Pro Gly Pro Arg Val Trp Gly Lys
                               -35                               -30

TAT CTC TGG AGA AGC CCT CAC TCC AAA GGC TGT CCA GGC GCA ATG TGG      100
Tyr Leu Trp Arg Ser Pro His Ser Lys Gly Cys Pro Gly Ala Met Trp
   -25                               -20                               -15

TGG CTG CTT CTC TGG GGA GTC CTC CAG GCT TGG CCA AMC CCG GGG CTC      148
Trp Leu Leu Leu Trp Gly Val Leu Gln Ala Trp Pro Xaa Pro Gly Leu
  -10                               -5                               1                               5

CGT CCT CTT GGC CCA AGA GCT ACC CCA GCA GCT GAC ATC CCC CGG GTA      196
Arg Pro Leu Gly Pro Arg Ala Thr Pro Ala Ala Asp Ile Pro Arg Val
      10                               15                               20

CCC AGA GCC GTA TGG CAA AGG CCA AGA GAG CAG CAC GGA CAT CAA GGC      244
Pro Arg Ala Val Trp Gln Arg Pro Arg Glu Gln His Gly His Gln Gly
      25                               30                               35

TCC AGA GGG CTT TGC TGT GAG GCT CGT CTT CCA GGA CTT CGA CCT GGA      292
Ser Arg Gly Leu Cys Cys Glu Ala Arg Leu Pro Gly Leu Arg Pro Gly
      40                               45                               50

GCC GTC CCA GGA CTG TGC AGG GGA CTC TRW BAC AAT CTC ATT CGT CGG      340
Ala Val Pro Gly Leu Cys Arg Gly Leu Xaa Xaa Asn Leu Ile Arg Arg
      55                               60                               65                               70

TTC GGA TCC AAG CCA GTT CTG TGG TCA GCA AGG CTC CCC TCT GGG CAG      388
Phe Gly Ser Lys Pro Val Leu Trp Ser Ala Arg Leu Pro Ser Gly Gln
      75                               80                               85

GCC CCC TGG TCA GAG GGA                                             406
Ala Pro Trp Ser Glu Gly
      90

```

(xii) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 62..172

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2
seq LLAVLLASWRLWA/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

AACTGGTGCG GCCGAGTGAC AGTTGACCGG TTTTAACCAA GTGACTGGTT CTAGCCACGT      60
T ATG TGC GGC CCA GCC ATG TTC CCT GCC GGT CCT CCG TGG CCC AGA GTC      109
  Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
    -35                -30                -25

CGA GTC GTG CAG GTG CTG TGG GCC CTG CTG GCA GTG CTC CTG GCG TCG      157
Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
  -20                -15                -10

TGG AGG CTG TGG GCG ATC AAG GAT TTC CAG GAA TGC ACC TGG CAG GTT      205
Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
  -5                1                5                10

GTC CTG AAC GAG TTT AAG AGG GTA GGC GAG AGT GGT GTG AGC GAC AST      253
Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
    15                20                25

TCT TTG AGC AAG AGC CCG GGG      274
Ser Leu Ser Lys Ser Pro Gly
    30

```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 71..235

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2

seq SLLLLSTALNILA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

ACATATCTTT GCAATTGTGA ACATTCAATC ATTTTCAACA CACGTTCATG GTTAATATTT      60
CTAGGAAACT ATG CAT AGA AGA AAA CTT CCT TTA ACC AAT AAA AGG CAA      109
      Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln
      -55                    -50                    -45
CTT CAA AAA MCA TTG AGT AAA TTC ATA TTC AGT GAT GAA TTG TTT AGA      157
Leu Gln Lys Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg
      -40                    -35                    -30
AAT ATT CTC TTT AGT TTA AGA ACA TTA AGG ATG ATA CTA TCA CTA CTT      205
Asn Ile Leu Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu
      -25                    -20                    -15
CTG TTG AGC ACT GCA TTG AAT ATC TTA GCC TGC CAA ATA AAT GAA GAA      253
Leu Leu Ser Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu
      -10                    -5                    1                    5
CTG GGG
Leu Gly
      259

```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 182..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

AAAACGCCGG GAGCTGCGAG TGTCCAGCTG CGGAGACCCG TGATAATTCG TTAAC TAATT      60
CAACAAACGG GACCCCTTCTG TGTGCCAGAA ACCGCAAGCA GTTGCTAACC CAGTGGGACA      120
GGCGGATTGG AAGAGCGGGA AGGTCCTGGC CCAGAGCAGT GTGACACTTC CCTCTGTGAC      180
C ATG AAA CTC TGG GTG TCT GCA TTG CTG ATG GCC TGG TTT GGT GTC CTG      229
Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
      -15                    -10                    -5

```

AGC TGT GTG CAG GCC GAD HYG
 Ser Cys Val Gln Ala Xaa Xaa
 1 5

250

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq LCLVCLLVHTAFR/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AAGAGCCTGT GCTACTGGAA GGTGGCGTGC CCTCCTCTGG CTGGTACC ATG CAG CTC	57
Met Gln Leu	
CCA CTG GCC CTG TGT CTC GTC TGC CTG CTG GTA CAC ACA GCC TTC CGT	105
Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr Ala Phe Arg	
-15 -10 -5	
GTA GTG GAG GGC CAG GGG TGG CAG GCG TTC AAG AAT GAT GCC ACG GAA	153
Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp Ala Thr Glu	
1 5 10 15	
ATC ATC CCC GAG CTC GGA GAG TAC CCC GAG CCT CCA CCG GAA CGG	198
Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro Glu Arg	
20 25 30	

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq ILLCSVAVXLSPS/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

CATAGGGTTT CGAAAATTAT CCACACTTTC TATGGTAATA GAATCTGATA TGGTTCAC TC      60
TTGGTGTTGT ACATTCTGTG GGTCTGGGTA AATGTATA ATG TTA TGT ATC CAC CAN      116
                               Met Leu Cys Ile His Xaa
                               -30

KAT AGG ATC ATA CAG GAC AGT TTC ATT GCC CTA AAA ATT CTC TTA TGT      164
Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala Leu Lys Ile Leu Leu Cys
-25                -20                -15                -10

TCT GTC GCT GTA TSM CTG TCT CCC TCC GAG CCC CTG GCG CCG      206
Ser Val Ala Val Xaa Leu Ser Pro Ser Glu Pro Leu Ala Pro
                -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

AAGGAGC ATG GGT GGT TTT TTT CCC CCT ACC GAG GTC CGT GAG GTG TGT      49
Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys
                -35                -30                -25

GCT AAC CAA GGG GCG GCT CAC AAC CGT GAC AGA CTG CCA TTC CTG AGT      97
Ala Asn Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser
                -20                -15                -10

```

```

CTC TTC TGG CCA TGG GCC CCC GGA GCC GTG AGC GTC GGG CAG GCG CGG      145
Leu Phe Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg
      -5                      1                      5

TAC AGA ACA CCA ACG ACA KSA GCG CCC TCA GCA AGC GTT CCC TGG CCG      193
Tyr Arg Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro
      10                      15                      20

CGC GCG GGT ACG TGC AGG ACC CCT ACG                                220
Arg Ala Gly Thr Cys Arg Thr Pro Thr
      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq HLWILLLFSCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

ACTTCCCTAT TATTCCTGAA ATG AAA TTA TTT TAC AAC CAG CTC GTT TCA GAA      53
      Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu
      -30                      -25                      -20

ACA AAA CAT GAT TTT GCA CAT TTG TGG ATT TTG TTG TTA TTC TCA TTT      101
Thr Lys His Asp Phe Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe
      -15                      -10                      -5

TGT TGG ATG TCT AGA AGC TTT TTT TTT TTT                                131
Cys Trp Met Ser Arg Ser Phe Phe Phe Phe
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 111..170
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLFFHILFHSCFS/HL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ACCTTTAAGA TTACCTGTAT AATAAATGTG TGCAGACACC ATCCAAAAG GTGTAAAAAA 60
TTGCAAAGGA AAAATAAATA CTGGCCAACA CAGTGTCTT AAAAGTACCC ATG CCT 116
                                         Met Pro
                                         -20

AGT GAG TCC CCT CCC TTG CTG TTC TTT CAC ATT CTG TTC CAT AGC TGT 164
Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His Ser Cys
      -15                      -10                      -5

TTC TCC CAC CTC TTG 179
Phe Ser His Leu Leu
      1

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..221
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLCSALAWQQSLS/GK
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATAAACAGGA AAGCACT ATG TCT TCA ATG TGG TCT GAA TAT ACA ATT GGT 50
              Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly
              -65                      -60

GGG GTG AAG ATT TAC TTT CCT TAT AAA GCT TAC CCG TCA CAG CTT GCT 98

```


Gly	Val	Lys	Ile	Tyr	Phe	Pro	Tyr	Lys	Ala	Tyr	Pro	Ser	Gln	Leu	Ala	
	-55						-50					-45				
ATG	ATG	AAT	TCT	ATT	CTC	AGA	GGA	TTA	AAC	AGC	AAG	CAA	CAT	TGT	TTG	146
Met	Met	Asn	Ser	Ile	Leu	Arg	Gly	Leu	Asn	Ser	Lys	Gln	His	Cys	Leu	
	-40					-35					-30					
TTG	GAG	AGT	CCC	ACA	GGA	AGT	GGA	AAA	AGC	TTA	GCC	TTA	CTT	TGT	TCT	194
Leu	Glu	Ser	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Leu	Ala	Leu	Leu	Cys	Ser	
	-25				-20					-15					-10	
GCT	TTA	GCA	TGG	CAA	CAA	TCT	CTT	AGT	GGG	AAA	CCA	GCA	GAT	GAG	GGC	242
Ala	Leu	Ala	Trp	Gln	Gln	Ser	Leu	Ser	Gly	Lys	Pro	Ala	Asp	Glu	Gly	
				-5					1				5			
GTA	AGT	GAA	AAA	GCT	GAA	GTA	CAA	TTG	TCA	TGT	TGT	TGT	GCA	TGC	CAT	290
Val	Ser	Glu	Lys	Ala	Glu	Val	Gln	Leu	Ser	Cys	Cys	Cys	Ala	Cys	His	
		10					15					20				
TCA	AAG	GAT	TTT	ACA	AAC	AAT	GAC	ATG	AAC	CAA	GGA	ACT	TCA	CGT	CAT	338
Ser	Lys	Asp	Phe	Thr	Asn	Asn	Asp	Met	Asn	Gln	Gly	Thr	Ser	Arg	His	
	25					30					35					
TTC	AAC	TAT	CCA	AGC	ACA	CCA	CGG									362
Phe	Asn	Tyr	Pro	Ser	Thr	Pro	Arg									
	40					45										

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq FVRFLGFVSCLQS/D?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TAGCTATTTT	CAGCGCTT	ATG	GCT	CTG	TTC	TTG	GAG	TTA	TTT	CTA	AAT	TCT	
		Met	Ala	Leu	Phe	Leu	Glu	Leu	Phe	Leu	Asn	Ser	51
				-25						-20			
TAT	TCT	CTT	TTG	TTT	GTA	AGG	TTT	CTT	GGC	TTT	GTT	TCC	TGT
Tyr	Ser	Leu	Leu	Phe	Val	Arg	Phe	Leu	Gly	Phe	Val	Ser	Cys
	-15					-10					-5		99

TCT GAT CCC ATT TGC TCT TTT TTT TTT TTT
Ser Asp Pro Ile Cys Ser Phe Phe Phe Phe
1 5

129

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 114..185
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq LMAGSSSLGAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATACTTCAAA	TCTTGAATTA	AATGAAGAAA	TTTATTTTAC	TGATTCTCTT	GAAATAAAGA	60
GAAATGAAAA	TTTTCCAAAG	GATTATGTGA	AATTTTCAGA	TGAAGAAGAA	TTT ATG	116
					Met	
AAT GAA GAT GAG AAG GAA ATG AAG GAA ATT CTA ATG GCA GGA AGT AGT						164
Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser Ser						
	-20		-15		-10	
TTA TCA GCT GGA GTT AGT GGG GAA GAT AAA ACC GAG ATA TTG AAT CCC						212
Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn Pro						
	-5		1		5	
ACT CCA SCG ATG GCC AAA TCT CTG ACC ATA GAC TGT CTG GAA TTG GCA						260
Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu Ala						
10			15		20	25
TTA CCC CCT GAA CTG GCT TTT CAA CTT AAT GAA TTA TTT GGT CCT GTT						308
Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro Val						
	30		35		40	
GGT ATT GAT TCA GGG TCT CTA						329
Gly Ile Asp Ser Gly Ser Leu						
	45					

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 167..229
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.8
 seq IIPLIXXLSLCLC/LW
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

CTATACGTGA TAAGTGAATA AAATGTGTCA GAGTGTACTA CTTAGAATTT TCATAGATTG   60
TAAAGATTTT CTATATATTT ATTTGAATTG GTAATTGGTT ATGAGCAGTT TGGTGTAGCT   120
GTTTTTAATT GTACAACAAT TAAGATATCA CCTATATTCT CGAAGA ATG GGA TCA       175
                                   Met Gly Ser
                                   -20

TTC CTT CTA GGA GGG ATT ATC CCT TTA ATA NNT TTN CTT TCT CTT TGT       223
Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu Ser Leu Cys
      -15                      -10                      -5

CTT TGT TTA TGG TGG AGA ATA ATT                                     247
Leu Cys Leu Trp Trp Arg Ile Ile
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 277..369
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.8
 seq VCLLCSGCSCAWS/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ACGAGTGTTA CAGAGGAGAT CTGGTTTCTG GAGGTCTCCA GGATGGGGCT GTAGCCTAAA   60
AGGAAGACTA TGTGAGGCAG CAGGCAAGCA GCAGCAAGTG GAAAGGCTTG GAGATGTGGA   120
GGACGTTATA TGGTACTCAG AGAGCAGCAG TACATGGATG GCAAGTGTGG CGTTGTGCTG   180
CCACCCACTT CCCCATGCCA AAAGCATATA ACTGCTAATC AGTTACCGCA TTTTTTGCTG   240
CCGAATTCGT AAGCAGCCCC AAGAGTTCTC AACAGG ATG CTT CAG GTG GCC ACT   294
                               Met Leu Gln Val Ala Thr
                               -30

ACT AAT TAT TTG GAG TTG GCA CGT GAG GTT AAA CCT GTT TGT CTT CTT   342
Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val Lys Pro Val Cys Leu Leu
-25                      -20                      -15                      -10

TGT AGT GGG TGT TCC TGT GCC TGG AGC GTA GGA TGT GTG TKG GAG TCG   390
Cys Ser Gly Cys Ser Cys Ala Trp Ser Val Gly Cys Val Xaa Glu Ser
                      -5                      1                      5

GAG TCA GAA   399
Glu Ser Glu
      10

```

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ATTACTTTGT CTAGATCAGG AGATGCTAGT ATATTCTTAG CACTAAGACC CCTCTGAAAT   60
CTTGTCCAAC ATTTAGCCAC CCAGRAGTTG TKCTTTACTA CACCTTTGAG GGTTATGCCC   120
TGTACATGTG CAGCTTAGGG GTTCAAGGAC AATCTCTTTA CACATTTTGG GGTT ATG   177
                               Met

```

TTC TGT CTA GCT CCT TTC TTT TTA GCA CTC TGC TTC CCA AAA TCT ACC 225
Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser Thr
-15 -10 -5

TCA CAG CCC CAA AGG 240
Ser Gln Pro Gln Arg
1

(2) INFORMATION FOR SEO ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 236..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq QCLLCISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 65:

TCCTCTTTGC	TGTTTTTCATC	AAGATAGTAG	AGCACATCTT	CTTCTCACAG	ACTACAAC	60
TGTGGTTTCAG	CACGAGGCAG	TAGAGGAAAG	TGCCTCGACT	GTGGGAGGCT	TGGSCAARAT	120
CCAAAGACTT	TCTCTCCTTG	TTGCTGGAGT	CGCTAAAAGA	ACAGTTTAAT	AATGCCACAC	180
CCATCCCCAC	CCACAGTTGT	CCCCTATCTC	CAGACCTCAT	TCGCAATGAA	GTAGA ATG	238
					Met	
TCT GAA AGC AGA TTT CAA CCA CAG AAT CAA GGA GGT TCT CTT CAA CTC						286
Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln Leu						
-30		-25		-20		
CCT CTT CAG TGC CTA CTA TGT TGC ATT TCT CCC CCT GTG TTT TGT GAA						334
Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys Glu						
-15		-10		-5		1

```

GGT AAC TGG TTA TCT TAC TTT TAT GTG CTT CCT GGA TTT GTG TGT GAA   382
Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys Glu
      5                      10                      15

TTA CAT AAA CTG GGT ATT TCT TGT TTA ATC CCC CTT TTC TCT GTC TCC   430
Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val Ser
      20                      25                      30

CCT TTG GCA GCC TGG ATG GTG   451
Pro Leu Ala Ala Trp Met Val
      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

ATGGAGCAGA GGTCCAGCTG TGGTGAGGAT TGGCACAGTC GTGCTTGTGG GACTCCTCCT   60

TGGTCCAACT CTAATGCTCA ACCTACACCA TCACCCCTGT GCTTGCTCCT CTA ATG   116
                                     Met

CCT AAG CAC TGT CAT TCC TTT ATC ACT AGT AGT TGC CTG TTG GGT TTG   164
Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly Leu
      -20                      -15                      -10

CTC CAT TTG TCC TCA CAG TTT AGC TGC CCT GGA AGG AAA CTC CAC CCT   212
Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His Pro
      -5                      1                      5                      10

GCT CAG AGA CAC ACT GAG GCT GAG ACC CAA GGG AGG CCC CTC TCT GAC   260
Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser Asp
      15                      20                      25

AGG   263
Arg

```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 166..222
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

ATCTCTCCTT TTTTCCTGTA ACTGTGCTGG TTTTGTTTTG GTCTTCCTCT CATACCCGTT   60
TCTGCATTTC ATCTTTTCTT TCTATTGTGA CTTCAATTCA TTTTTTTTTT AACCTTATCT  120
TTTGTTTCTC TTGTTTATCC CATCCTTTTT GATAAAATCC ATCGC ATG TGT CTT CTT   177
                                         Met Cys Leu Leu

TTT TYC TTT ATT TYC TTT CCT TTC CTT TTY CCT TTT TCT TTC TCC CAA   225
Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe Ser Phe Ser Gln
-15                      -10                      -5                      1

ACT TTT TCC TTT TCA CAG CAT TGG AAC ACG GGA GGT AGT CAC CCA GAA   273
Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly Ser His Pro Glu
                    5                      10                      15

GAA CTT GAG CGG CCT GGT GCC CAT CCG AGA CTT AAG GCT AGA CCC CAG   321
Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys Ala Arg Pro Gln
                20                      25                      30

CCT CCT CTG TTC CAT CCC TTT ATT AGC TCT   351
Pro Pro Leu Phe His Pro Phe Ile Ser Ser
        35                      40

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 30..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LLVASGXAEVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

ACGCGCAGAC CCAGCGCCGA GCCCGAGCC ATG GCG TCC GAG CGG MTC CCT AAY      53
                        Met Ala Ser Glu Arg Xaa Pro Asn
                        -25                      -20

AGG CCC GHC TGT CTG CTC GTR GCC AGC GGC GMC GCC GAR GGT GTG TCG      101
Arg Pro Xaa Cys Leu Leu Val Ala Ser Gly Xaa Ala Glu Gly Val Ser
      -15                      -10                      -5

GCC CAG TCC TTC CTC CAS TGT TTC ACG ATG GCC AGC ACC GSC TTC AAC      149
Ala Gln Ser Phe Leu Xaa Cys Phe Thr Met Ala Ser Thr Xaa Phe Asn
      1          ..      5          10          15

CTG CAG GTG GCC AYC CCT G GK GGG AAA GCC ATG GAA TTT GTS GAT GTG      197
Leu Gln Val Ala Xaa Pro Gly Gly Lys Ala Met Glu Phe Val Asp Val
                20          25          30

ACT GAS AGC AAT GCA CGC TGG GTG CAA GAC      227
Thr Xaa Ser Asn Ala Arg Trp Val Gln Asp
      35          40

```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 160..234
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

AATTTCAAGT TGT CATAAAA GTTCAGACAA CCATCACTGG ACCTACAGAT TGAGTGATTA      60

```



```

TTATAGTGGG GATGTCCTTG GGTTAGTAAG CCTAAAGGAA GTAATTCTG TTAAGGAGA 120
TGTTAGTGGC CATTGTCATC TTAATGTCAA TCTTATCAG ATG TTC CCA GAC TAC 174
                                         Met Phe Pro Asp Tyr
                                         -25

AAA CTG GGT GGG TCA TAT CTC TTA GCA TTT CAA CTG GTA TTT CTC AGA 222
Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln Leu Val Phe Leu Arg
-20                      -15                      -10                      -5

GCA ACT AGT GGC TCA TGT TCC AAA TAT AGA AGG CAT TTG CAT AAC ATC 270
Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg His Leu His Asn Ile
                      1                      5                      10

AAT GTT AGA CCT GGG CTT GTT AGA CTC TTG GGC TCA TGT ATA CAA AAG 318
Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly Ser Cys Ile Gln Lys
                      15                      20                      25

CAA CCT GGG 327
Gln Pro Gly
                      30

```

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 44..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLLXLXLLLIALE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

AAATGTGTAC ACGCCCAGCT TCCTGCCTGT TACTCTCCAC AGT ATG CGA AGA ATA 55
                                         Met Arg Arg Ile
                                         -25

TCC CTG ACT TCT AGC CCT GTG CGC CTT CTT TTG TDT CTG CWG TTR CTA 103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Xaa Leu Leu
-20                      -15                      -10

CTA ATA GCC TTG GAG ATC ATG GTT GGT GGT CAC TCT CTT TGC TTC AAC 151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
-3                      1                      5                      10

```


(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 215..292
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

AAAAAGTACT GAGAGGTTGA TGGGACTGTT CGATTAGCTC CTCTGAGAAG AAGAGAAAAG   60
GTTCTTGGAC CTCTCCCTGT TTCTTCCTTA GAATAATTTG GATGGGATTT GTGATGCAGA  120
AAAGCCTAAG GGAAAAAGAA TATTCATTCT GTGTGGTGAA AATTTTTTTGA AAAAAAAATT  180
GCCTTCTTCA AACAAGGGTG TCATTCTGAT ATTT ATG AGG ACT GTT GTT CTC ACT   235
                               Met Arg Thr Val Val Leu Thr
                               -25                               -20

ATG AAG GCA TCT GTT ATT GAA ATG TTC CTT GTT TTG CTG GTG ACT GGA   283
Met Lys Ala Ser Val Ile Glu Met Phe Leu Val Leu Leu Val Thr Gly
          -15                      -10                      -5

GTA CAT TCA AAC AAA GAA ACG GCA AAG AAG ATT AAA AGG CCC GGG   328
Val His Ser Asn Lys Glu Thr Ala Lys Lys Ile Lys Arg Pro Gly
          1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 150..269
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ATTCTTTCCT TCTCATATCT ACAATTGCTC CTTTCTAGTT CAGTTCCTA GTACAGCTGG   60
AGTGATTATT KSKKTTAAA AAATGCAAGC ATAAAAAGA AATAACAAA TAGTTAAATC   120
ATGTTATTCT TTTGTTTACA CTGTAATGA ATG TCT TCC CCA TTG CTT GTA GAA   173
                               Met Ser Ser Pro Leu Leu Val Glu
                               -40                               -35
CAA AGT TCT ACA AAG TCT CCC AAA AGC TGG TCC TGG TCC TTT CTA GCT   221
Gln Ser Ser Thr Lys Ser Pro Lys Ser Trp Ser Trp Ser Phe Leu Ala
      -30                               -25                               -20
TTC TCT TGC ATA AGT CTT CTT TTT ATT TTT TTC AGC ATT GCA AAT TCT   269
Phe Ser Cys Ile Ser Leu Leu Phe Ile Phe Phe Ser Ile Ala Asn Ser
      -15                               -10                               -5
TCC CCC TGC GGG
Ser Pro Cys Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 96..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq IPLLLLFFHLSFL/NS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

AGAACAAAGT TTAGAATGAT ATGTTTATGC CTGTGACAT TTATCTTGTT AGATTATGCT   60
CACTAAGCCA TTGGGGTGTT TGGGGAATTT GATCA ATG TAT CTT TTC TGT CTC   113

```

Met Tyr Leu Phe Cys Leu
-25 -20

TTT TCA GTT TCG AAA ACT ATC CCT CTG CTG CTG CTT TTC TTC CAC TTG 161
Phe Ser Val Ser Lys Thr Ile Pro Leu Leu Leu Leu Phe Phe His Leu
-15 -10 -5

TCT TTT CTC AAT AGC TTG 179
Ser Phe Leu Asn Ser Leu
1

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 170..217
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq CLLILKFLSPAET/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ACAGAGTTCA CTTCTAGGAT ATTCCTTCCC AATCTTCACA GTCACCTCAT AGTCACTATG 60

AGGATTACAT GAGTKAATAT TTGTAAAAAG CGTTCAGGAG AGTGCTTGCT TCACATCAAA 120

TACTATATAT ACTTGTTAAA TAAATAGATC TCATTCACCC CACGAAACA ATG ATC GTT 178
Met Ile Val
-15

TGT CTC CTG ATT CTC AAG TTT TTG TCT CCA GCA GAG ACB TCT ATT CTG 226
Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr Ser Ile Leu
-10 -5 1

AGC TCC ATA GCT ACA TAT GGG GCT TTT TAT TTC ATA GTT CCA CTG GAG 274
Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val Pro Leu Glu
5 10 15

GTT TCA CAA ATC CTT CAA ACT CAG 298
Val Ser Gln Ile Leu Gln Thr Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 180..254
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.7
seq LILCFLFILHTHT/HT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

ACAAACTGGT TACCCTGCCA CATGTATACC CCCTTCTCCC CATTCTCACT TCCTCGTTAG    60
ACGAAATGAT CATCCAGTGA AGCCATAGAT TATATTGGCC ATCTAATATC AAACCATATT    120
GGTCTCATTT GAAATCTTT CATGATGCTT TGTGGTATTC ACAGTGAAGT TTAGATTCC    179
ATG GAT AAG AGC ATC AAG TCC TCT ATA ATC TGG TCT CTG ATT CTC TGT    227
Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25                -20                -15                -10
TTT CTT TTT ATC CTG CAC ACA CAC ACA CAC ACA CAC ACA CAC ACA CAC    275
Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His Thr His
      -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 283..390
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.7
seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

ACAGACCTCT TTGAAAATCT AATGAGAGCC ATAGACTTCA CCCTAAAAAA ATATATATGC   60
ATAAAAAGTT TAAATATAGT TTGGAGAGTA ACGCACCTTC CCCTAAAGCA ATTCCTAAAC  120
CTCATTATAA GGATCTATAT TCTATAGTTC AGTTCTGCAT TTTAATGTC TTCTATATTG  180
TCTCATGCTA GAATAGTCAT TATATCTTCA TATGTAATAT TTAAAGTGTG AATTATCATC  240
TAACACTTCC TGTCTTCTGT CCCCCAAATC TATACTTCTC CC ATG TTC TTT ATT   294
                                   Met Phe Phe Ile
                                   -35

TTC ATT AAT GGC TTT ACW CTC CTT CTA ATG ACC CTA GCC ATG AAA CCC   342
Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu Ala Met Lys Pro
      -30                -25                -20

AGG CAT CCT ATT TTT GAC CTC TTG CTA TTG CTK RAB HTA TCT AAT CAA   390
Arg His Pro Ile Phe Asp Leu Leu Leu Leu Leu Xaa Xaa Ser Asn Gln
      -15                -10                -5

TTG CCA GTT ACG GGG                                           405
Leu Pro Val Thr Gly
  1                5

```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LWPFLTWINPALS/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

AC ATG TGC CCT AGT CTG GAA GAG GCT CCC AGT GTC AAG GGG ACT CTG   47
  Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu
    -60                -55                -50

CCC TGC TCA GGA CAA CAG CAG CCT TTC CCG TTT GGA GCC TCA AAC ATC   95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile

```

-45	-40	-35	-30	
CCA CTA CTC CTG GGC AGG AGC AGA AAG GTG GCT CGA GGT GCA CCG GTC				143
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val				
	-25	-20	-15	
CTG TGG CCA TTT CTC ACT TGG ATA AAC CCT GCA CTG TCC ATC TGT GAC				191
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp				
	-10	-5	1	
CCC TTA GGA TCC TGC GGA TGG CAG				215
Pro Leu Gly Ser Cys Gly Trp Gln				
5	10			

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 287..337
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAGCTCCAAG GCAGGAAGAG AATTGGGCAT CGGGTACGAA CCTGGCAGCT CAGGAGTCGG	60
GGCTCCACTC ACCCCACACA AAAAGATGAA AAAAGCGCAW AGAGCTCAAT GCATTGATTG	120
GTTTGGCTGG GGACAGCCGG AGAAAGAAGC CCAAGAAAGG CCCAAGCAGT CACCGCCTGC	180
TTGCGACTGA GCCTCCCGAC TCATACTCTG AGTCCAGCTC CGAAGAGGAA GAGGAATTCTG	240
GTGTGGTTGG AAATCGCTCT CGCTTTGCCA AGGGAGACTA TTTACG ATG CTG CAA	295
	Met Leu Gln
	-15
GAT CTG TTA TCC GCT CTG TGG TTT TGT CAT CCT TGC TGC CTG TGT TGT	343
Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys Leu Cys Cys	
	-10
	-5
	1
GGC CTG TGT TGG CTT GGT GTG GAT GCA GGT TGC TCT CAA GGA GGA TCT	391
Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln Gly Gly Ser	
5	10
	15

GGA TGC CCG
Gly Cys Pro
20

400

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

AAAATGTCCT CCACAGCTTT GCCCAGTGGG ACACATGGCT CCTGACATAC GTAACCCAGG    60
ATGGGATGCC TTGTTGGAGT CTCTCAGATA TGGAGCAAAA TGGGCCATGT GCAGTCAAGA    120
CGCCATCTAM CCTGGGCAGC TTGCCTAAGC CTCGAGGGAC CTGCCA ATG ATG GAT      175
                                     Met Met Asp
CTG AGA CCT CTT CTG TCC CTG GCT GCC TAT CTG TCT GGT CCT CAT CAA      223
Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly Pro His Gln
   -15                               -10                               -5
GAA CCC AGT GTT CCC ACC CGA GAT GGA GAC GTG AAT AAT CTT CCT AAG      271
Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn Leu Pro Lys
   1                               5                               10                               15
CCT AAT CCT GCC AGA AGC GTG AAG CAA GGG GGA ATH TGG AAG GCG GAA      319
Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp Lys Ala Glu
          20                               25                               30
CAG GAA AGA GTG GAA GTG GAG                                          340
Gln Glu Arg Val Glu Val Glu
          35

```

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 147..203
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLPGLPLVRTSFS/HF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

AGCGGTCAGA GGATGCCCTC TTCGCCCTGT GAGCAGCTCT GTGGTTTGCC TCCCCAGATG    60
GCGGGTCCCC GCTTGCACCC CGTGGACACC GGGCACTGGC CACTCCTACA TCCCCAGCTC   120
CACACGGCCT GCACACCTGT GTTTCC ATG GAA ATG CCA CCG TGT CTG CTC CCA    173
                               Met Glu Met Pro Pro Cys Leu Leu Pro
                               -15

GGC CTC CCA CTA GTC AGG ACC AGC TTC AGC CAC TTC TTT TCT CTG AGT    221
Gly Leu Pro Leu Val Arg Thr Ser Phe Ser His Phe Phe Ser Leu Ser
-10                               -5                               1                               5

GGT GGG ACA ACT ACA GCC AGA GGG                                245
Gly Gly Thr Thr Thr Ala Arg Gly
                               10

```

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 19..93
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq GLAMLHVTRGVXG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ACATGCGCAG GAGGCTCA	ATG ACA GTC GAG CTT TGG CTA AGG CTC CGG GGA	51
	Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly	
	-25 -20 -15	
AAG GGT CTA GCC ATG CTG CAT GTG ACC CGG GGG GTC TRG GGG TCC AGG		99
Lys Gly Leu Ala Met Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg		
	-10 -5 1	
GTC CGA GTA TRG YCA MTG TTG CCC GCG CTC CTC GGG MCC CCC MGG GCC		147
Val Arg Val Xaa Xaa Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala		
	5 10 15	
CTC TCA TCG MTG GCA GCC AAA ATG GGG GAK TAT CGC AAS ATG TGG		192
Leu Ser Ser Xaa Ala Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp		
	20 25 30	

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 7..78
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq LLILLCSSPPDRV/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

ACAAAC ATG TCT ATA GAA GAT TTT GTG AAT AGA AGC ATA CTT CTG ATC	48
Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile	
	-20 -15
TTG CTC TGT TCT TCC CCA CCT GAT AGG GTC AGC TAC AGA GCC AAG GTT	96
Leu Leu Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val	
	-10 -5 1 5
TTA CAC TCA TTG CTT CAA TTG CCC GCC CAG	126
Leu His Ser Leu Leu Gln Leu Pro Ala Gln	
	10 15

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..91
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq FALLFLFLVPVPG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AAGTCTCAGC GTGGGGTGAA GCCTAGCAGC T ATG AGG ATC CAT TAT CTT CTG	52
Met Arg Ile His Tyr Leu Leu	
-20 -15	
TTT GCT TTG CTC TTC CTG TTT TTG GTG CCT GTT CCA GGT CAT GGA GGA	100
Phe Ala Leu Leu Phe Leu Phe Leu Val Pro Val Pro Gly His Gly Gly	
-10 -5 1	
ATC ATA AAC ACA TTA CAG AAA TAT TAA TTG CAG AGT CAG AGG CGG CCG	148
Ile Ile Asn Thr Leu Gln Lys Tyr Xaa Leu Gln Ser Gln Arg Arg Pro	
5 10 15	
GTG TGC TGT GCT CAG CTG CCT TCC AAA GGA GAA AGG	184
Val Cys Cys Ala Gln Leu Pro Ser Lys Gly Glu Arg	
20 25 30	

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 217..255
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq MCLLTALVTQVIS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

AATGCCAGTG TCAGCTTCTC TCCGAAACT GGGTAATACG AAATGGTCTT TATTGGTTGT   60
GAACACTCGA GCTGAGAAAC ATTTTAGGAT CTTTGTGTCT TTTGTGATGA TTTTGTTCCT  120
GRAAGRWGGA AASCTGTCTA AAAATATTCA AGTGTGCAAC CAAGGATTTA GATGAAGCCA  180
GCAAACAAAG GAATCATGTA ATCAGGACCT GAGCGA ATG TGC TTA CTC ACG GCG   234
                               Met Cys Leu Leu Thr Ala
                               -10

TTA GTT ACA CAG GTG ATT TCC TTA AGA AAA AAT GCA GAG AGA ACT TGT   282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
      -5                      1                      5

TTA TGC AAG AGG AGA TGG CCC TGG NGC CCC TCG CCC CGG ATC TAC TGC   330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
  10                      15                      20                      25

TCA TCC ACC CCA TGC GAT TCC AAA TTC CCC ACC GTC TAC TCC AGT   375
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..129
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq GLALVAGTPPSRS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ATCTGGCGCG TGGTCTTGCA TTCCTACTT GGTCCTGTTC GTGGCGCCGC GCCTCCGGGT   60
GTTGGGGAGT CCGGG ATG ATG GGG AAT CCG GGG CTC GCC CTA GTC GCG GGG   111
      Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly
      -15                      -10

ACA CCG CCT TCC AGG AGC TGT CCC CAG GCA AAC TCA CAG ACG CGG   156
Thr Pro Pro Ser Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..299
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq PCVSLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

ATAACCCATA TAGTAGTTAA GCCATTGTGG TGAGGGTGTT TGAAACCCAG CTATCCTATG   60
TAATGCTATT TCCAGGGGAA AAATATTCCC AATTCCAGGT AAAAGATCAG AAACAGATAT  120
CACCTGSAWT TTGTTCCACC TTCACCCAG GCTTCAGCTA TACTTAGGTA TTACTCTCTG  180
GTCCC ATG AAC CAT CTC ATG CCT TTG ACT GTG CTG CAC TCA GTG CTT GAA   230
    Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu
        -35                      -30                      -25

ATG CTC CGC ACA CCC CGC ACA CCT CCC TGG CCC TGT GTA TCC CTT CTA   278
Met Leu Arg Thr Pro Arg Thr Pro Trp Pro Cys Val Ser Leu Leu
        -20                      -15                      -10

TGG GCG CCC AGA GSA TTT GCT TCC TCT TGC TCT CAA GCA TTT ACC ACT   326
Trp Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr
        -5                      1                      5

CTG CAN KGC AAT TGC TTG CTT ACT AAT CCA TCT CCC ACA CTA GAT TGT   374
Leu Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys
    10                      15                      20                      25

GAC CTC CCT GAG GGC TCA GAA ATA TTA AAT TCT TCT CTG TAT CCT CAT   422
Asp Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His
        30                      35                      40

TGC CTA CTC AGT GCT TGG AAC ACA CGA CAC TCA ACA   458
Cys Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
        45                      50

```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 13..84
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ATTATTATTT TT ATG GGA CAT GTT GTG TTT GGG GAT ATA AAA AAT AGT TTA 51
Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu
-20 -15

TTA KGT TTA AGG GCT TCG CAG CTT AGT GAG GGA GAC ACA TGR VTG AAM 99
Leu Xaa Leu Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa
-10 -5 1 5

TVA TGT CCA BRT ATG RTG AGA GGT AAA CAC ATA TCC TAT 138
Xaa Cys Pro Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr
10 15

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 48..290
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq FLSLLXSVSETPG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

ACTTCTTCCC CGGGTCTCCG AAGCCGCTAG GGAAGCGCAA GTGGGCC ATG GCT GGC 56
Met Ala Gly

-80

GGG Gly	AGG Arg	CGG Arg	GAT Asp -75	TAC Tyr	AGC Ser	CAG Gln	CTC Leu	TTT Phe -70	GGC Gly	CGC Arg	GGC Gly	CCC Pro	GGT Gly -65	CGG Arg	CTC Leu	104
TCG Ser	CGA Arg	GCG Ala -60	CGA Arg	GCC Ala	TCT Ser	GTT Val	GTG Val -55	CGT Arg	TGG Trp	TCT Ser	CCC Pro	CGG Arg -50	GCA Ala	ACT Thr	GCT Ala	152
TGC Cys -45	CCT Pro	GCG Ala	CCA Pro	CCG Pro	AGC Ser	CTC Leu -40	CCG Pro	GAT Asp	TTA Leu	AAG Lys	CGG Arg -35	CAG Gln	GAG Glu	CTG Leu	GTT Val	200
AGC Ser -30	CGG Arg	ATA Ile	GAA Glu	TGT Cys	GGG Gly -25	TGC Cys	CGA Arg	GGG Gly	CCG Pro -20	GTG Val	GGG Gly	GCC Ala	ACC Thr	GCA Ala	GAC Asp -15	248
TTC Phe	TTT Phe	CTG Leu	TCC Ser -10	CTG Leu	CTC Leu	TDC Xaa	AGC Ser	GTC Val	TCT Ser -5	GAA Glu	ACC Thr	CCT Pro	GGC Gly	AGC Ser 1	CTG Leu	296
CGG Arg	RGA Xaa	AAC Asn 5	GAT Asp	CTT Leu	TTC Phe	TTC Phe	GTC Val 10	TCT Ser	CAG Gln	CTT Leu	ATT Ile	TGG Trp 15	GGC Gly	CGG Arg		341

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 207..263
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LWCFSFSFISFSL/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ATCCTCCATA	GCTATATCCA	TTTCCTGGGA	CATGGGTTGG	CCCAAGAGGG	AATGAGAAGG	60
ACCTGCGATT	GCACAGGAAA	TTCTGGGGCA	CATTTAACGT	TAAATCATT	AGCTTCTGCC	120
AATAAATCCA	TTACTGTTAA	TTACACTGAG	ATGGCCAACG	ATCTGCTGAC	AATATTCCTT	180
CATTGATTTT	CATTCTCAGT	GAATCG	ATG	TTC	TGG	CNT
				GGC	TCT	CTT
				TGG	TGT	
				Met	Phe	Trp
				Xaa	Gly	Ser
				Leu	Trp	Cys
						233

-15

TTT CAT TCT TTC ATT TCT TTC TCC CTG TCC TCA TCA CGG 272
 Phe His Ser Phe Ile Ser Phe Ser Leu Ser Ser Ser Arg
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..225
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FLLTFFSYSLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AGGCNNNCGG ASCSGGGCTG GAGAGCGGCS NCCACTGCGG ATCTCGGAAG GAAGAAATGA 60
 TGTAATCAC TCATSSAVAC TTAAAGGTCN NNGTGAGAM GGAAGGTCAG GMAGAAC 117
 ATG GCC TGG CCA AAT GTT TTT CAA ABA GGG TCT CTG CTG TCC CAG TTC 165
 Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
 -35 -30 -25
 AKN BAT CAT CAT GTT GTA GTG TTC CTG CTC ACT TTC TTC AGT TAT TCG 213
 Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
 -20 -15 -10 -5
 TTG CTC CAT GCT TCA CGA AAA ACA TTT RGC AAT GTC AAA GTC AGT ATC 261
 Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
 1 5 10
 TCT GAG CAG TGG ACC CCA AGT GCT TTT AAC ACG TCA GTT GAG CTG CCT 309
 Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
 15 20 25
 GTG GAG ATC TGG AGC AGC RAC CAT TTG TTC CCC AGT GCA GAG 351
 Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 466 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 380..436
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq WILAVGLSLPSSS/XI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

ACTCTCTTCT ACTGGAATGG TACCCTTGTT GACTGACTCA TGTATAGCTG CTTGGCTTAA   60
TGGTAGACCA GATATTCAGG TCCTCTGAGA CAGGCCCTG ATGACTTTTG CAACTACATC  120
TTTCAMCACA GCCTGCCTTG CATTTTGGAC TCTAGCAACA CTGAAATACA TGTCATTTCC  180
CAAGGCATGT TAAGCTGTTT CTATTCTCTA GGCTCTCCCT TTTTCCTAGA ATGCCCTTTT  240
CCTCTAGGCT AATGTCTTTC TCCTTTAAAT TAGTCATCTT CAACAAAGGC TACCTTGACC  300
TTCTCTTGAC TTTGCCACAT TCCTGCTGCT GCCTTCCTTC CATGGCCTTT GTCACGCTAT  360
ATGGTAATTG ACAGGTTCC ATG ATC TTG AGG AAC TTA TGG ATT TTA GCA GTG   412
          Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val
                    -15                      -10

GGT CTT AGC TTG CCA TCT TCT TCA MCC ATC AAG TTT CAT TTC TCT CTT   460
Gly Leu Ser Leu Pro Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu
          -5                      1                      5

TAC TCA
Tyr Ser
    10

```

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 267..371

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVFS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

ACAATCAGTT TGCCAATACC TCAGAAACAA ATACCTCGGA CAAATCTTTC TCTAAAGACC   60
TCAGTCAGAT ACTAGTCAAT ATCAAATCAT GTAGATGGCG GCATTTTAGG CCTCGGACAC   120
CATCCCTACA TGACAGTGAC AATGATGAAC TCTCCTGTAG AAAATTATAT AGGAGTATAA   180
ACCGAACAGG AACAGCACAA CCTGGGACCC AGACATGCAG TACCTCTACG CAAAGTAAAA   240
GTAGCAGTGG TTCAGCACAC TTTGGT ATG TTG ACT GTT AAT GAT GTA CGT TTC   293
                Met Leu Thr Val Asn Asp Val Arg Phe
                -35                      -30

TAT AGA AAT GTC AGG TCC AAC CAT TTC CCA TTT GTT CGA CTA TGT GGT   341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
   -25                      -20                      -15

CTG TTA CAT TTA TGG CTT AAA GTC TTT TCT CTT AAA CAG TTA AAA AAA   389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
   -10                      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 111..179

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9
seq LFLNLCILAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ATTAATTTTA ATTTTCATTG TCAATATTTT GAGCTTAGAA CATTTATGGT ATAAAAATTT   60

```

AAACTAATCA AAGTTGTGTG ATGATTTC CG GGAATTATTA TTGAAAGCCT ATG AAT	116
Met Asn	
TTA AAA CCA GGT TTA CCA TGT AAT TTG TTT TTA AAT TTA TGT ATA CTA	164
Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys Ile Leu	
-20 -15 -10	
GCC TGV CCT TTC TCC AAG CAA ATT ATT GAA CTA TTA GAA TAT GTT AGT	212
Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr Val Ser	
-5 1 5 10	
TAT CAT CCT TGT GTC TTA GTA TAT AGT GAA TAC AGM AAC ATC AGC ATT	260
Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile Ser Ile	
15 20 25	
GTA TAC ACT CTT	272
Val Tyr Thr Leu	
30	

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 43..162
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAWGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ACCAGAGAGA GTGGCGCGAG CTGCGTTTTT CGGCCAGAGG AC ATG ATG CAG GGG	54
Met Met Gln Gly	
-40	
GAG GCA CAC CCT AGT GCT TCC CTT ATT GAC AGA ACC ATC AAG ATG AGA	102
Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg	
-35 -30 -25	
AAA GAA ACA GAG GCT AGG AAA GTG GTC TTA GCC TGG GGA CTC CTA AAT	150
Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn	
-20 -15 -10 -5	
GTA TCT ATG GCT GGA ATG ATA TAT ACT GAA ATG ACT GGA AAA TTG ATT	198
Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile	

	1	5	10	
AGT TCA TAC TAC AAT GTG ACA TAC TGG CCC CTC TGG TAT ADY GAG CTT				246
Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp Tyr Xaa Glu Leu	15	20	25	
GCC CTT GCA TCT CTC TTC AGC CTT AAT GCC TTA TTT GAT TTT TGG AGA				294
Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg	30	35	40	
TAT TTC AAA TAT ACT GTG GCA CCA ACA AGT CTG GTT GTT AGT CCT GGA				342
Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly	45	50	55	60
CGG				345
Arg				

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 274..330
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq PXXLLILAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTATTTGTT AAATGCTACA AGAGTGA CTG GGATCATAAG TGTTACGGGA GTTTGGCAAA	60
GAAGCAGGAG GTAGTTAGTG TAACTGTTAA TGTGATTATA AGACTAATAC ATTTTGTKGG	120
RAGATAACTT ACCAAGTTTG GTTTGTGGAA AATTTGGATT GAGAAGGAAA TTGTATGTTT	180
CCGTTAGAAG TAGAACAACA ACAACAAAAT ATCTCCCATC ATTTGTTTGG TACTATCTGG	240
CCTCCCCAGT GCTGCTTGGG AGAATCATGA AAC ATG ATG AAT CAA ACA CAT CCT	294
Met Met Asn Gln Thr His Pro	-15
TRM RTG TTG CTC ATC CTG GCA CAT ATT ACA CAG AGT TGC CCA TGG GCC	342
Xaa Xaa Leu Leu Ile Leu Ala His Ile Thr Gln Ser Cys Pro Trp Ala	-10 -5 1
CAT GTA GGA GCA GCT CCA TCT GCC CTT CTA ATA CAT ACG TGG GAR CTG	390

His Val Gly Ala Ala Pro Ser Ala Leu Leu Ile His Arg Trp Glu Leu	
5 10 15 20	
AGG GGG TGC TCG TAT TTG AAA CTG TTT TTG GTT ATG GTG CTC ATA TTT	438
Arg Gly Cys Ser Tyr Leu Lys Leu Phe Leu Val Met Val Leu Ile Phe	
25 30 35	
GAA ATG CTT	447
Glu Met Leu	

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq GLVLLLSLAEILF/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AGTCCTAGTC AGAGTTTCT GTGAAGGCAA GGGC ATG GGG TTG CCG GAG AGA AGA	55
Met Gly Leu Pro Glu Arg Arg	
-20 -15	
GGA TTG GTC CTG CTT TTA AGC CTA GCT GAA ATT CTT TTC AAG ATC ATG	103
Gly Leu Val Leu Leu Leu Ser Leu Ala Glu Ile Leu Phe Lys Ile Met	
-10 -5 1	
ATT CTG GAA GGA GGT GGT GTA ATG AAT CTC AAC CCC GGC AAC AAC CTC	151
Ile Leu Glu Gly Gly Gly Val Met Asn Leu Asn Pro Gly Asn Asn Leu	
5 10 15	
CTT CAC CAG CCG CCA GCC TGG ACA GAC AGC TAC TCC ACG TGC AAT GTT	199
Leu His Gln Pro Pro Ala Trp Thr Asp Ser Tyr Ser Thr Cys Asn Val	
20 25 30 35	
TCC AGT GGG TTT TTT GGA GGC CAG TGG CAT GAA ATT CAT CCT CAG TAC	247
Ser Ser Gly Phe Phe Gly Gly Gln Trp His Glu Ile His Pro Gln Tyr	
40 45 50	
TGG ACC AAG TAC CAG GTG TGG GAG TGG CTC CAG CAC CTC CTG GAC ACC	295
Trp Thr Lys Tyr Gln Val Trp Glu Trp Leu Gln His Leu Leu Asp Thr	
55 60 65	

AAC CAG CTG GAT GCC AAT TGT ATC CCT TTC CAA GAG TTC GAC ATC AAC	343
Asn Gln Leu Asp Ala Asn Cys Ile Pro Phe Gln Glu Phe Asp Ile Asn	
70 75 80	
GGC GAG CAM CGG	355
Gly Glu Xaa Arg	
85	

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 305..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATCAGTCTGT GGAGACAGGT GAGCACGAAC TTCTGAGACA GGTGTGGGTG CGAGGGTCGG	60
GAGGGTCATG GGATTGGGAC CGAGGTGTGA GGAGGGAATC TGCAATTCCT TGCTACACAG	120
AGCGCTGGCA ACTTCTGACA GGCTGTTTCT GGGGTATGGG CTGCCTCGGG TTGTTGCTGT	180
TACAAGGAAA GAAAAGAGTT CCCCTGCCCA CCGCCTCCCA GCCACTGGGC TACCTCCTGG	240
CAGGAAATTT GCAAACCTGAG TTTAACAAGT TAGGATCAGC AGAGGGTAGA GGAGGGCCTG	300
GCAG ATG TGG GGT CTA GAA GAG GAC AGG AGT TAT CAG GGS CTC CGG CCA	349
Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro	
-25 -20 -15	
TTG TGC TGG GCT TTG CTG TAC AAT TGT TTC TCA AGC AGT TGT GTY CCT	397
Leu Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro	
-10 -5 1	
GTG GCT TTG GTG	409
Val Ala Leu Val	
5	

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 129..383
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq ALLASLGIAFSRS/RA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

AGTAGCGGAC ATTTTGTTC TGTCAGGCTG TCCCTGGCCG GGGTTCTGTA ACGCTTGTGT    60
GGGCCGCAGG TGGAGGTGTT GGGAAAGCGC GGAGGAGATG TTGTCCCCAG TGTCCCGAGA    120
CGCGTCTG ATG CTC TGC AGG GAC GGA AGT GCC TGC GTC CCC CGA TCG AGA    170
      Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg
      -85                      -80                      -75

CGC CTG CCG CTC CCG GCA GCT GTC CGC GCC CAC GGT CCT ATG GCG GAC    218
Arg Leu Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp
      -70                      -65                      -60

TGN NCG GAC TCC GCG CGG GGC TGT GTG GTC TTT GAG GAT GTG TTT GTA    266
Xaa Xaa Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val
-55                      -50                      -45                      -40

TAC TTC TCT CGG GAA GAA TGG GAG CTT CTT GAT GAT GCT CAG AGA CTT    314
Tyr Phe Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu
      -35                      -30                      -25

TTG TAC CAT GAT GTG ATG CTG GAG AAC TTT GCA CTT TTA GCC TCA CTG    362
Leu Tyr His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu
      -20                      -15                      -10

GGA ATT GCA TTT TCC AGA TCA CGT GCA GTC ATG AAA CTA    401
Gly Ile Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 100:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 61..228
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ATACCTAATG ATAACACAGT ATCTCTTCGA ATTTGTACTA TTGCAGAACA TTTAGAAACA      60
ATG CTT ATT ACT CGK TTA CAG TCT GGT ATA GAT TTT GCA ATC CAG CTT      108
Met. Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
   -55                      -50                      -45

GAT GAA AGC ACT GAT ATT GGA AGC TGC ACA ACA CTT TTA GTT TAT GTC      156
Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
  -40                      -35                      -30                      -25

AGA TAT GCG TGG CAA GAT GAT TTT TTG GAG GAT TTT TTG TGT TTT TTA      204
Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
          -20                      -15                      -10

AAT TTA ACC TCA CAC CTA AGT GGA TTA GAT ATT TTT ACA GAA TTA GAA      252
Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
      -5                      1                      5

AGG CGC GGG
Arg Arg Gly
    10
  
```

261

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 191..304
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.7

seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

AACTCTGCAG GGCCTCCAAG GCCAGGCTTC AGGGCTGGGA CTCAGTCCTG AGGCACTGGG    60
GAGCCATGAG GGGCTGTGGC AGGGAGGGGC AGGGTGTGGA AAGACTCCCC TGGGGCCATG   120
GTGGAGATGT GCTGAGGTCT TCTCCCTGAT CGTCTTCTCC TCCCTGCTGA CCGACGGCTA   180
CCAGAACKAG ATG GAG TCT CCG CAG CTC CAC TGC ATT CTC AAC AGC AAC       229
          Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
                    -35                               -30

AGC GTG GCC TGC AGC TTT GCC GTG GGA GCC GGC TTC CTG GCC TTC CTC       277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25                -20                -15                -10

AGC TGC CTG GCC TTC CTC GTC CTG GAC ACA CAG GAG ACC CGC ATT GCC       325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
                    -5                      1                      5

GGC ACC CGC TTC AAG ACA GCC TTC CAG CTC CTG GAC HKC ATC CTG GCT       373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala
          10                15                20

GTT CTC TGG
Val Leu Trp
      25

```

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 190..273
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLLFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

CTCTTGTTAA CCTGTCTTTT GCTATAGGAG TGTCAGACCC TTATGAGGGG AGAGGAGAGA    60
TATCATACTT TTTCTACCTC TACACTTTTA ATATCATTA TTTTCTAACA ATGCCCAAAT   120

```

CTTCAGTACA CCTCTCTCTC CTGAACCCTA TACTTGTACA GCAACTTTCT ATGTGACATT 180
 TCTTCTTAA ATG TCT AAT AAG TAT ATC AAA CCT AGC ATG TCC CCA GGA AAC 231
 Met Ser-Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn
 -25 -20 -15
 ACT GAT CAT CTT TTC CTA CTC TTC CCC CGA AGT TGT TCC TCC CTC GTC 279
 Thr Asp His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 263..334
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFLLPPXPP/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ATATGTGTAA TGTCTTTATT CCTTAGACTA TGGTCTCCGT GGAAGATTAC TGATACTCCC 60
 ACTAGTATTA ATAACAATGT TAGGTAACAT TACTGAATGT TTACTGAGTG CCAGGTAATG 120
 TTCTAATTGC TTTACATGTA TTAGGCTATG TATTCCTCAC ATGAACCATA TGAAAGAGAT 180
 ACTCTTATTG TTGTCATTTT AGAAGTGAAG AACTGAGGC ACAGAAAACCT TAAGTAATTA 240
 GTCCAATTCA TACAGGTAGT AT ATG GTA GAA CTG AAG CAG TTG GGC CCC AGG 292
 Met Val Glu Leu Lys Gln Leu Gly Pro Arg
 -20 -15
 TCT TTT TTT TTC TTT CTT TTT CTT CTG CCG CCG RCT CCT CCA ACC GGG 340
 Ser Phe Phe Phe Phe Leu Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 17..94

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LILPALFFFPLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AAACACCTTC TCAGTG ATG CCT TAC GTC ACC ATC CCA TAT ATA ATA GTG TAC    52
          Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr
          -25                               -20                -15

TCA CTC ATT CTA CCT GCC CTC TTT TTT TTC CCT CTC CAC TGT ACT TTT    100
Ser Leu Ile Leu Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe
          -10                               -5                      1

CAC GGT CTA ACA TAC TAT ATA TCA TGT GTT TGT TCA TTA TCT CTA CCC    148
His Gly Leu Thr Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro
          5                               10                      15

ACG
Thr
                                                                151

```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 247..321

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LLLCMDLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

AATTATTTTA TAAACTTCT GGCTGGATT AAATACTAGG CAGTATTCCA AGGGATGATA    60

```

```

AAATGTTTTT ACAAACCTTAA TTAGACCCAT TTTTGTAAAT AACTTTATT ATACATGTGC 120
TATGAGGATT AACTTTTGCC TCATAAAAGT ATTCTGACAG GTGCTTTGCA CAGAGTAAGT 180
CCGCCAAAGT GGACGTTCTC ATATGTAATT CTGAGCTTAC TCATACTGGC CAGGAAGGAC 240
GTGCAC ATG CCA CCT TTG GCA GCT GTG ATG GGG AGC CTG CCT CTG CTC 288
    Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu
      -25                -20                -15

TTG TGC ATG GAC CTT CCA CAT TCT GTC CTG TCC AAC TGG 327
Leu Cys Met Asp Leu Pro His Ser Val Leu Ser Asn Trp
  -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..248
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq EFLELGFPNSW2/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

ACAGCTAGAA TATGTTGGAT TCAGGAGCTT GTCCATTATT TGTAGGTAAA AAAAGCTGCA 60
CGTAGATTTG ACTTCAACTC CGTAAAAAAG ACAGCTGTAT TTTCCGTCCA ACTGGAATTG 120
TTGAATCACA CTGCATAGCT GCCCAAAAAGA GAGTGTTTGG TCTTGAACCT TCTATACTTT 180
TATAA ATG TTA CAA ATT CCC GAA AGA AGG GAA TTT CTT TTT CTG GGG TTT 230
    Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe
      -20                -15                -10

CCT TCA AAC TCT TGG CCC CAC AGG 254
Pro Ser Asn Ser Trp Pro His Arg
  -5                1

```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq FLITLFCCCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
ACATGTATCT GTTGGCTATT TGTATATCAT CTTTGCATCT TTGGATAA ATG TTC TTT      57
                                   Met Phe Phe

GTC CAT TTT TTA ATC ACT TTA TTT TGT TGT TGT GTT GTA GTG GGG TTT      105
Val His Phe Leu Ile Thr Leu Phe Cys Cys Val Val Val Gly Phe
-15                -10                -5                1

TTT GGC CAT GAT CAT TCA TTT ATC TCA CAG TTC ATT CTT GTT ACT TGG      153
Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu Val Thr Trp
                    5                10                15

GCC AGG GCA GGG
Ala Arg Ala Gly
                20
```

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ATCAGTGTAT TTTTTTATA GATTTAAAT ATACCTGAAA ACTTTTCTAG GAAGAATAAT	60
TATTCATGGA AAGAGCATTG TA ATG GCA TGT TTT GGG GAG AAA AGA CAT GCC	112
Met Ala Cys Phe Gly Glu Lys Arg His Ala	
-25 -20	
AAG TCT TGT TTA CTA CAT TTA AGA TGT TTA CAA CTA TAC TGG GCT GCT	160
Lys Ser Cys Leu Leu His Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala	
-15 -10 -5 1	
CGG	163
Arg	

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 279..362
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109;

AATAAACCTT	ACTTTAACAG	AATTTAACAG	ATATCTCTTT	AAAAAACTGC	TTTAATGTTT	60
TTACCTTCTA	TCTTCTTTTT	CTCCAGCTTT	ATCCTGACAG	RGAAGTTAGC	ACTAATTAAT	120
CTATTTTCTC	TTCCCCCTCT	TTTTTCCCTT	GTGTGTGTCT	TTTCTGCCTT	CATCTACCCC	180
ASTGAATTTG	TTCAGCATTT	TGGCTCACTC	ATTTCTTCAG	CTAACTACAG	CTTACTACTA	240
CAGCCACCAC	TACTAGAGCC	ACTCCTGTCT	CATCCTGG	ATG GTT GAC AGA GAT GAA	296	
				Met Val Asp Arg Asp Glu		
				-25		
AAC ATC TTG CTA AAG CAA ATA TAC AGY CCC CTT TCA CTG GCT CTC CAG	344					
Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro Leu Ser Leu Ala Leu Gln						
-20 -15 -10						
TCC TCC TGC TGT CTT TGC TTG ACC TCC TGC	374					
Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys						
-5 1						

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 115..174
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ATAAAATTTA CAGAAAAGTT GCAAAGAAGA TAGAATTTCT GCTTAGCTTT TGCCCCAATT   60
TCCCCTTGGC CACCCCTCCC TCTTTGTGTT TGTATCTTTT TTTTCTGAG CCAC ATG   117
                                     Met
                                     -20

AAA GTA AAG CCG CCT TTT GTG TCT GTG TCA CTC TGT GTG TGT GAC TGT   165
Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp Cys
                      -15                      -10                      -5

GTA AGG GGT AGC ACA CTT ACA TGG AAC AGG TTA CTG CGT GTG GGA GGG   213
Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly Gly
          1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 68..184

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ATGGCTAACA TATTCTTTTT TTTTCTCTG TAGTAGTTTT TTGAAAGAAG AAATAGGCTA   60
TTCTAGC ATG ATC TCA TCC TGT GGA GTT AAA TAC TTG TTT TCA CAT GCC   109
      Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala
                -35                      -30

TCC TTA TTT TTT ATG GTA GGG AGT ACA GGA AGT TTA ATA CTC TTA ACT   157
Ser Leu Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr
-25                -20                      -15                      -10

TCT TGT TTC TAT ACC CTT GTT TCA TCA ACC TTT CTT CAA AAA CTC TCT   205
Ser Cys Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser
                -5                      1                      5

TCT TTG CTC TTG ATA TTA TTT ACC GAA ACA AGT GTY CTT ATG TTA AAA   253
Ser Leu Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys
      10                15                      20

ACA TTT GTA GCT AAT TCT TGC TGT WAA TTG TGG TCT CAC AAT TGT ATT   301
Thr Phe Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile
      25                30                      35

AAT TTC TTC AAA AAG GTC CKG CCT TCT TAT TGC KGC AGC AGT CTA CTC   349
Asn Phe Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu
      40                45                      50                      55

TTC CTG GCC GTA CCT AGG
Phe Leu Ala Val Pro Arg
                60

```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 174..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq SFLCNFLVSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

AGAAGGGGGT GAAAGGAGTA ACTGCTATAT TTAGAAGGAG GTTAAGGATA GCAATTGATT    60
TTAAGGGTGG GGCTAGGGAA CTTGTCTTTA AAATCCTGCA TTTGCACAGC AAGCACAGTT    120
CGTATTGAGA TTTTGCTATT TGGAAGTGTG AGGGAGGTAT AGGATGCTGC CTA ATG      176
                                     Met
                                     -20

GGA GGT GGG ATH GCA GAG AGT TTT CTA TGT AAT TTC TTG GTA TCA CTT      224
Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser Leu
          -15                      -10                      -5

TCC CTC TCT TTC CTC CAT GGC CGG                                     248
Ser Leu Ser Phe Leu His Gly Arg
          1                      5

```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 265..363
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LAYFLCCQGVIFG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

CTATTCTCA TTGTCTGTCT GGTTTTCCAT CCCCTCACA TGTGGTGACC AGCACCTGGC    60
CCGCCACGGC AGCCAGGAGG CATTTGTAA GCGAATAATC GAGACAGGGA AGAGGAGTGG    120
AGTTGGCTGC TCCAGACTCT GCTTAGTTTT CCTTTCTCAA AGTTCTCCCT CCTGTGTCCT    180
AGCCGGGGAA TTAGCTAAAA TGGAATTTTC TTTGGTGATC AGGTATCCTT CTGATGAAGA    240
GAAGAAAGGC CTAAACTCCC AGGC ATG GAT GCA TTA GAA AGA GGT AGT CTT      291
          Met Asp Ala Leu Glu Arg Gly Ser Leu
          -30                      -25

AGA AAT GAG CAG GCG TTG GTT ATT TAT GCA GGA CTG GCA TAC TTT CTS      339
Arg Asn Glu Gln Ala Leu Val Ile Tyr Ala Gly Leu Ala Tyr Phe Leu
          -20                      -15                      -10

```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 78..194
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq SLWFLPLPTHVYT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTGCTTGAAC CTA	CTGTCT	TGTTTTTGTC	TTCTGTGAG	TTCAAGGACA	GGAGCAGTGC	60
TTAACACACA GTAGGTA	ATG GAA TAT	TTG TTC CAG CAG	CCT GGA CAC	TCA		110
	Met Glu Tyr	Leu Phe Gln Gln	Pro Gly His	Ser		
		-35		-30		
AGG GGA GAA GCC	AGG GCT GCT GCT	GCC TCT CTG	GAA ACC CTG	TCT TCC		158
Arg Gly Glu Ala	Arg Ala Ala Ala	Ala Ser Leu	Glu Thr Leu	Ser Ser		
	-25	-20		-15		
CTT TGG TTT CTG	CCT CTC CCA ACC	CAC GTG TAC	ACA CAT ACA	CAT GCC		206
Leu Trp Phe Leu	Pro Leu Pro Thr	His Val Tyr Thr	His Thr His	Ala		
	-10	-5		1		
AAC						
Asn						209
5						

(2) INFORMATION FOR SEQ ID NO: 115:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 283..327
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3
seq SSMLITILSFIFA/LG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

ACCACAGTCA CTGTCACATT ATTCTGTTTT GTATTTTATT TACAGCTCTT ATAATTATCC   60
GAACTTACAA ATTTATTTTC TTGTGTTTTT TCCGCCTGCT CCTCCACTTC ATTCTGTAAT  120
ACTATAGTTC ACTATAATAC TTCTAGTTCC TAGGACTGGA ATTATGTGTC TGGCACATAG  180
TAGACAGTAG ATGTTTCATTG AATGAATGAA TGATTCAAAT GAGATTTAAA TAGCAACAGT  240
CCTGACAGAA TGGTAAATTT CCACAATTAA GATGGTCTGT TA ATG GTA TCA TCA   294
                                   Met Val Ser Ser
                                   -15

ATG TTG ATA ACT ATT CTA TCG TTT ATT TTT GCC TTA GGG TAC CAC ACA   342
Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu Gly Tyr His Thr
  -10                -5                1                5

GCT TCT TAT CCA GTC TCC CTT CAT CCA CTC TCC TTT TTC CTA CAC       387
Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe Phe Leu His
              10                15                20

```

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 316..369
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ACAGTACTTG GAGGTATTCT AAAGGCAGAC ATACTTTATC TGAGCAGGTG CTTTGGCGT    60
GGTCCTGCCA AGAAAGAAAC AATGGCTTAG ATGACGTCTA TTCTAAGGCC TCAAGGCTTG    120
CACCCCTGCC ATGCTAAATA CAGATGCGCT CCTCCACCAA GAGAATCCCC TCTGCCCTCT    180
GCCATCTCAG CCCCAGGCCA GCTCAGCTGC CCATGACCTG TGTGCAAAGC AGGGGGCGGG    240
ACAAACAGCT ATCGCCTTTG GCCTTCCCTT TGCTCCTGAC AGCGCTCTCA AACCTGGAGC    300
AGTCAAAGGT CCAAG ATG CCT TTG TTC ACT ATG AAC CTG GTG TCA GCT CTA    351
          Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu
                    -15                      -10

GCG TCC TCA GCA RCA GGG CAG CGT GGA GCA GGG CCA GCC CTC TGG CAC    399
Ala Ser Ser Ala Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His
   -5              1              5              10

TTG TGT
Leu Cys
                                         405

```

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..226
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

CTTGCTTGTA AACATAAGCA TGTATTATTA CCTAGGCTTT GAATTTCAAA ATACGGTGTA    60
AACTACTCAT GGTAATATAG ATCTTGTTAG ACAAACGTTT ATGTAAAAA ATG ATC TGC    118
          Met Ile Cys

AAG CAT TAC TGT ATA AAG AAA AAT AAC CTG GAT TAC TTG AAT AGA ATG    166
Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu Asn Arg Met
   -35              -30              -25

GTT TAC AGT GGT CAG TTA AAG TTG ATA CTT CTT CTA CAT TGC AGT ATT    214

```

Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His Cys Ser Ile
 -20 -15 -10 -5

AGG GTT TTT TTT TTT TTT
 Arg Val Phe Phe Phe Phe
 1

232

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 232..390
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTTGAGAA GTGCCCTCCT ATACTTAGAG AAAAGGAATA TCCATATCTC TGAAGACACA 60
 GGGACACAGA GAGAATCTGA ACACACAGCC TTGGTAGGAT TCCTTCGGTT TATCATCATT 120
 AGATCATAAC CCCYTTTGTC MAGTCCTATT TCTCCARGAC TGCCTCCTTC TTCATTAAAC 180
 CTTGCATAAA AACTCACAAA TTTAACCATT TATTGGATT CTTATTCCT T ATG AAA 237
 Met Lys
 ATT CCT GTG TGG CAT AAA ACG TGC TTT TTA AAA TCT GAA AGT TTT TCT 285
 Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser Phe Ser
 -50 -45 -40
 CCT GAT AAT TTA TCT GTT AGT TTG CCT TGT AGA CCT AGC CAG GTA CCC 333
 Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln Val Pro
 -35 -30 -25 -20
 TCA CAG GGG CAA GGA AAA TCT TTT CTC CTC CTA CAA CTT ATA CAT GAG 381
 Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile His Glu
 -15 -10 -5
 GAT AAA GCC ATC CAG AAT GAA GCT ATT TTC CAG CCT TCT CTG CAG CTG 429
 Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu Gln Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 133..189
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPAFA/LS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

AGTCTGGGGG TGACATTGCA CCGCGCCCCT CGTGGGGTCG CGTTGCCACC CCACGCGGAC   60
TCCCCAGCTG GCGCGCCCCT CCCATTTGCC TGTCTGGTC AGGCCCCCAC CCCCTTCCC   120
ACCTGACCAG CC ATG GGG GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG   171
          Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala
                   -15                      -10

TTC DGC CCG GCC TTC GCG CTT TCH TTG ATC ACT GTG GCT GGG GAC CGT   219
Phe Xaa Pro Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg
      -5              1                      5              10

GGG
Gly                                     222

```

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 80..181
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq LWSSCWLAFLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

AAGATGAAGA GGAGGCDGTG GCAGTGGTGG AAGAAGAGGC GCGGCGGCGG GGGTAGGGAG      60
CCTGGAAACG CGAGCGGGG ATG GTA GGT GGT TTG GAC CCG CCG GGC CGC CGT      112
      Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg
                        -30                        -25

CGT TTC CAG AAA GGG TTT GAC TGG AGG AAC CTC TGG AGC AGC TGT TGG      160
Arg Phe Gln Lys Gly Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp
      -20                        -15                        -10

CTG GCT CCT CTG GCT GAT GGC ATG TTG AGG TAC ATG GGC CAG CVG CAG      208
Leu Ala Pro Leu Ala Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln
      -5                        1                        5

CGA NGG GCA TCC AAT CCA GAG GGG TCC ACT CTA GAG GCC AGG CCA CCA      256
Arg Xaa Ala Ser Asn Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro
      10                        15                        20                        25

GCA CCA TRG GCC AGT GTG TCA CCA AGT GTA AKH MTC CCT CAT CGA CCC      304
Ala Pro Xaa Ala Ser Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro
      30                        35                        40

TGG GCA GCA AAA ATG GAG ACC GTG AGC CCA GCA ACA AGT CRC ATA GCA      352
Trp Ala Ala Lys Met Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala
      45                        50                        55

GGC GGG
Gly Gly
      358

```

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:


```

ATAGAACTAC TCGGGAACCT CAAAATCAGT AGATTGGAA GTGATTCAAA GCTAAACTTT      60
TTCCTTGGCC CTCCKTGTGT TCTAATTGCT TTGCAAGTGT AAKACTAGG ATG TCC AAG      118
                                   Met Ser Lys
                                   -20

ATG CCA GTT TTT GCT TCT TTG TTA GTT GTC AGC TGC TTT TAT CAA ATT      166
Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe Tyr Gln Ile
      -15                      -10                      -5

TCA GGC CGC TGG      178
Ser Gly Arg Trp
      1

```

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 136..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AACAAAGAGA CACAGACAGG GGA CTGTCAG CYGGYACCGG AGGMCGGAC AACGAGTTAT      60
CAGCAACTSA AAGCACCTGA BGGGCCGCAC ATTCCANCCC CAGCCCAGTC CTCGTCTCTC      120
ACGCCAGCNC CAAGC ATG TSA GTA ACC CAA CTT CTC CCT TTC TCC TCC CCA      171
      Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro
      -15                      -10                      -5

GAC TCT GCG GGT CCT TTT CTG TCC CCT TTC TCT      204
Asp Ser Ala Gly Pro Phe Leu Ser Pro Phe Ser
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..102
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ATG GGG AAA GCA TGG CAA GAG ATG AGG GTG GAA TGG GGG GCA GAC AAG	48
Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys	
-30 -25 -20	
GGG AAT GTC AGA AGC AGC TTC CAC TTT CTC CCC TGG GCA CTG GGA GCC	96
Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala	
-15 -10 -5	
ATG GCA AGT TCA GAG CAG GGG AAG GAG AGG TCC AAC TTG TGC TTT AGG	144
Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg	
1 5 10	
AAG ACT CCT CTG GCT ATC ACG GGG AGA GGA ATT GCC AGG AGA CCA GGG	192
Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly	
15 20 25 30	
GGA GGT TGG ATG GGA ATG TGG GTG	216
Gly Gly Trp Met Gly Met Trp Val	
35	

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 2..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

A ATG AAA GTG ATG ATG AGG AAG AGG AAG AAA AAG GAC CAG TGT CTC CCA   49
  Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
    -45                      -40                      -35

GGA ATC TGC AGG AGT CTG AAG AGG AGG AAG TCC CCC AGG AGT CCT GGG   97
  Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
    -30                      -25                      -20

ATG AAG GTT ATT CGA CTC TCT CAA TTC CTC CTG AAA TGT TGG CCT CGT  145
  Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
    -15                      -10                      -5                      1

ACA AGT CTT ACA GCA GCT ACG                                     166
  Thr Ser Leu Thr Ala Ala Thr
                    5

```

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 254..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ACTGTTTTAG TGTTTGAAT ATCTTCTTCC AGAGTTTGAT GTATATGTAT CTTGGAGGTA   60

TATGTATTTT TAATTATATA AATATTTGAC CCTCTTTGCC TARTTTGTTT TATTCAC TTC  120

AACTTTGACC CTTTATACTT CTTTTTAAAT TTCACCTTCT TATGGTTGTT TTTCTACTTT  180

TCCTCAATGC CCTTTGTAAA ATTTTCATTT GAATCTATTA TTCTCCCTTG GACGTCTTAA  240

TTCCTTCTCT ACT ATG ACT TTT TCT TTC TTT TGT TTC TTT CCT GGG TTC   289
  Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe
    -35                      -30                      -25

AAG CCA CTC CTG TTT CAT TAC TTT CTT TTT WNK TCC TTT TCT ATT TKD   337
  Lys Pro Leu Leu Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa

```

	-20		-15		-10	
ACT CTK CTT TGG GGC TTG AAC TGT AAG AGG TCC TGG AAC ATA AAT TTG						385
Thr Leu Leu Trp Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu						
	-5		1		5	
AGA ATT GTT GSA TCA TAC AGT AGT GGT TAC						415
Arg Ile Val Xaa Ser Tyr Ser Ser Gly Tyr						
	10		15			

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..133
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGAGGCAACC ATG GCG GGA GGA ATG AAA GTG GCG GTC TCG CCG GCA GTT	49
Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val	
-40 -35 -30	
GGT CCC GGG CCC TGG GGC TCG GGA GTC GGG GGC GGT GGG ACA GTG CGG	97
Gly Pro Gly Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg	
-25 -20 -15	
CTA CTC TTG ATC CTC TCC GGC TGC TTG GTC TAC GGC ACA GCT GAA ACT	145
Leu Leu Leu Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr	
-10 -5 1	
GAT GTA AAT GTG GTC ATG CTT CAG GAA TCC CAA GTT TGT GAA AAG CGT	193
Asp Val Asn Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg	
5 10 15 20	
GCC AGC CTC GGG	205
Ala Ser Leu Gly	

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 58..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ACTTCCACGG GACCCACCAG CTAAATGCC GGCAGCCCTG GGACTTCTGG CCTCACA      57
ATG GTT GAG ATG ACT GGG GTG TGG CAG TGC CAA GCC GAG GCT GTG AAA      105
Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
      -30                      -25                      -20

GGC CTT CCA CCT TTA CTC TCG TGC TCG TGC CCT CCC CCA TTG TTA GGA      153
Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
      -15                      -10                      -5

GAA GGG CAT GCT CAG GCC AGC CCA TTA GCC CAG GAG GAG GAC AAG AAA      201
Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
      1                      5                      10                      15

CAC ACG GAG CAG ACA CAA GCC ACC TCA CCA ACC CAG CCT      240
His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 59..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

AATTTGCTCA CACCCAGCAG GCAGAGAAGG CAGCAGCAGG CAGGACCGCC ACCCTCCC      58
ATG CAA ATC ACC CCC GGG AGT GCA GCT GGG CTC CTC CCG CTC CTC CTA      106
Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
  -20                -15                -10

GGC AAT GCT CCT GGG GAG TCT GTT GGG GGA AGA TGC SAT CCA GGG TGC      154
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
  -5                1                5                10

TGG
Trp

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 152..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLTQLNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

AGAATTTTGC TGGAATTAA TATTAAATAC TCACTGGAAT TTATCTTTAC CAACTTTAGT      60
GGAATTCAGC CTATCTACAG CTCTCCTTTC CACTTTGTTT CTCAGAAATT CTCAGCAATG      120
GTTTCATGAA CCACTGGGAG GTCATTGCC T ATG ATT TTG TCC ACC TGG CTC      172
                               Met Ile Leu Ser Thr Trp Leu
                               -15

TTA CTT ACC CTT CAA AAC TCA GTA TTT ACA TCT TTC AGG ATA TCT CCC      220
Leu Leu Thr Leu Gln Asn Ser Val Phe Thr Ser Phe Arg Ile Ser Pro
-10                -5                1                5

AAC AGA ATA CAA AGT ATG CTA CCT CCC ATG      250
Asn Arg Ile Gln Ser Met Leu Pro Pro Met
  10                15

```

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..128
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

AAATCTCTTC TAATCCTCCT TAATGCATTT TG ATG GCT TTT CAT AGC TAT TGG      53
                                   Met Ala Phe His Ser Tyr Trp
                                   -30

GGA AAA AGT TTA CAA TCC TTT AAG ACG TTC ATG AGA GTC TGC ATT GTC      101
Gly Lys Ser Leu Gln Ser Phe Lys Thr Phe Met Arg Val Cys Ile Val
-25                -20                -15                -10

TTG GCC CTT TGC CAC ACA TCC AGA CCC ATG TCT TAC CAT GTT CCC CTG      149
Leu Ala Leu Cys His Thr Ser Arg Pro Met Ser Tyr His Val Pro Leu
                -5                1                5

GCT GCT GGC TCC CCA CTC ATG CAC TGG TCT CCT TGT AGT CCT GTG CCC      197
Ala Ala Gly Ser Pro Leu Met His Trp Ser Pro Cys Ser Pro Val Pro
                10                15                20

TTC ATT GGG
Phe Ile Gly
25

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 113..160
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq RFTLLPLVLHSQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

ATTCTCGTA AATGATGAGA TGGGGTTAAA TGGTTTTCGA GAAATATGTG AGAGGTAATG. 60
TGAAATAAGT TACTTTAAGA AGGCCTGGCC CTGGTAATGT CGTTACCAGC TG ATG AAG 118
                                         Met Lys
                                         -15

TTG CGG TTT ACC TTG CTG CCC CTG GTG CTA CAT TCA CAA AGC AGC TGT 166
Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser Ser Cys
          -10                -5                1

GTC. TTT TGG AAA GCC GGG 184
Val Phe Trp Lys Ala Gly
          5

```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 4..93
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACC ATG ATG ATC ATT CTG GGG TTT GCT TTT TGC CCT GGT CAC TTT AGG 48
Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg
-30                -25                -20

TTT AAT TTT ATT CCA TTC CTG GTC ATT TAC AGT TTT GTT CTG TCA TCT 96
Phe Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser
-15                -10                -5                1

CCC CAT ACC CAT CGA GAA CCC TAT TCT CCT GTG GCA GAC TTT AAT GAA 144
Pro His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu
          5                10                15

```


TGT AAC CGC AGT
Cys Asn Arg Ser
20

156

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 198..278
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9,
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

AACTTTGCCT GGGTGTCTTG CGTTCTGCAC ATTCCGGAGG ACCAGCTTCC CCATCAGAAG    60
TCTGACTCCA TGGAACCAG ATGGGGCAAC GGGGTGGTTC TAGTGCAGAC TGTAGCTGCA    120
GCTCCTCTCC ACCTCTAGCC TGCTCATTTT CAGCTCAGAA ATTCTACTAA TGGCGTTTTT    180
TCTTCCTGAA AAAGGAA ATG AAC AGG GTC CCT GCT GAT TCT CCA AAT ATG      230
          Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
          -25                      -20

TGT CTA ATC TGT TTA CTG AGT TAC ATA GCA CTT GGA GCC ATC CAT GCA      278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
   -15                      -10                      -5

AAA ATC TGT AGA AGA GCA TTC CAG GAA GAG GGA AGA GCA RRT GCA AAG      326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys
   1           5           10           15

ACG GGC GTG                                335
Thr Gly Val

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 195..239
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

AATATGTAAA TGTACTATAC AGAATTATAC ATAAAAGAGA AACTTTTCAT GTATGTAAGT    60
TTAAAAATGA AGTAAATGGG GGTTCAAAT AACATTARAA TTGGTTATGA GTTTTGGAAA   120
AGGAAATCAT ACTTGGCATT CTAAACTTAA TATTTCTTTG CAATGTTTAG GTATATGTGG   180
ATATTCCTGG AGCT ATG GAT TTA TTT CTT AAT TTG CCA CTT GTC ATC GGT    230
          Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly
          -15                      -10                      -5

ACC ATT CCT CTA CAT CCA TTT GGT AGC AGA ACC TCA AGT GTA AGC AGT    278
Thr Ile Pro Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser
          1                      5                      10

CAG TGT AGC ATG AAT ATG AAC TGG CTC AGT TTA TCA CTT CCT GAA    323
Gln Cys Ser Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
    15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

AAAATATTAA ATG GMA AAA AAT CAC AGA AAT AAA AAA TCC ATA CAT TTT	49
Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe	
-70 -65	
CCA CTG TGC ACC ATT CCA AGT AGM ATG MTG AAA TCT TGT ACT CTC CCA	97
Pro Leu Cys Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro	
-60 -55 -50 -45	
CTT CAG CGC ACC TGG GAC ATS MAT CCT TCC TTT GTC CAT TGG AWC CAA	145
Leu Gln Arg Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln	
-40 -35 -30	
GCC CGY CTA CAA TCC CCA CCG YCT AGT CAC TTA GTA SCC CTC TCG GTG	193
Ala Arg Leu Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val	
-25 -20 -15	
ATC AGA TCG ACT CTC GTG CTA TCC CAG TGC TTG TGT TCA AGG MAC CCT	241
Ile Arg Ser Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro	
-10 -5 1	
TAT TTT AGT GCA ATG ATG ACC CCA AAG TGC AAG AGT ATT GMT GCT GGC	289
Tyr Phe Ser Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly	
5 10 15 20	
AAT TCA GGT ATG CCA AAG AGA AAC TGT AAA GTG CTT CCT TCA AGT GAA	337
Asn Ser Gly Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu	
25 30 35	
AAG ATG MAA GTT CAC	352
Lys Met Xaa Val His	
40	

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 317..358
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

AGAGCAAAGC AGACAGAAAT TCCTCTGGTT CTGTAGAGCT GACAATTCAT TAATGTGAGG   60
TAGTCAATAA CAAATATATT TTATGTCAAG TGGTGRATGG DTYCDATTGA AGAAAAATGA   120
CTCAATAAGA GGAGAGAAAA TGATGGTATG TGTATGGTGG GTAGGTGTGC GTGATGCTGT   180
TTTGGATAGC GAGGCCTCCG ATTAGATGCT ACGTGAGCAG GGACCCAAAA GAGCCATGTG   240
TTTCATCTAC CTGGGGGAGA AGCCTGCTGG CAGATCCTGT TGAACACTCG TTACCTAAAT   300
CTCTTGCAAT GGCTCC ATG TCA TTT ATT GCT CTA GTG TAT TCT TCA CTA TCT   352
          Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser
                    -10                               -5

TTT CAG AAA GTG CCA GGG                               370
Phe Gln Lys Val Pro Gly
      1

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 93..158
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

ATAATATAGA TCTTTAATTT CTCTCAGCAA TGATTATAGT TCACAATGTG GAGGATTTAC   60
ATGTCTTTCA TTAAATTTAT CCAAAGTACT TT ATG GTT TTT GAT ACT TTA AAA   113
          Met Val Phe Asp Thr Leu Lys
                    -20

AGT AGA ATT GTT CTT TTT TTA AAT TCG RWT TTC CCA ATC ATT TGC AGC   161
Ser Arg Ile Val Leu Phe Leu Asn Ser Xaa Phe Pro Ile Ile Cys Ser
-15                    -10                    -5                               1

CGG                               164
Arg

```

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 68..244
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq IFLFSILLMSLRT/FH
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AAAGCACAGA TGGCAGTCCA TTCATTGAAG ATGGTTTTTT TCAAGGTGAG TGTGGTCTT    60
TTGCACA ATG CTT GAG ATG GAA ATG ACT TGG CTG AGA CTA TGT GAT GAG    109
      Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu
                -55                      -50

TGC TCC AGA TGG GGC ATG GCA TCG GCA TGG GGT AGG GGT GGA AAG CTT    157
Cys Ser Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu
-45                -40                      -35                      -30

CTT GGA GCT CAA GTA GCC CTT CAT CCT AGA AAC TGC AGC AAA GCT AAG    205
Leu Gly Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys
                -25                      -20                      -15

ATC TTC CTG TTC AGT ATT TTA TTA ATG TCT TTA AGA ACT TTT CAC TGT    253
Ile Phe Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys
                -10                      -5                      1

AAT TAT TTC AGA GGC AAT GGG    274
Asn Tyr Phe Arg Gly Asn Gly
      5                10

```

- (2) INFORMATION FOR SEQ ID NO: 139:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 104..154
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AACAAAGGAG GGAAGGGTTA GAGTGAGGTA CTCACCCAGA GAAGAGCTGT CCCGGCCTGG      60
GGGTCCCATT CGTCCCTTCT CTTTCTTGCC AAAGAGACGG CCT ATG GAT GAC TTG      115
                                   Met Asp Asp Leu
                                   -15
ATG CTC TTC TTC TTG GGG GCT TTG TGC AGA GAA TCT GGG GTG CCC TCA      163
Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser Gly Val Pro Ser
      -10                -5                1
CTG GGA AAG CAG GAG AGA ATG AGA GCA TAT GCT GCT GAG ATG CCC CCT      211
Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala Glu Met Pro Pro
      5                10                15
CTC CTC CCA AGT CCT TGT CCA CCC CCT TCT CAT CTT CCC AAG CCA GCT      259
Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu Pro Lys Pro Ala
      20                25                30                35
TCT CCC TGT CCC TAT CCC TTG NNC CTG CTG ACC TTC CCC GTG GGG GTC      307
Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe Pro Val Gly Val
      40                45                50
CCC CAT CTT CCA GGG ACC CGC CTG CAG TGC CAA GGC CTG GGT CAT TCT      355
Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly Leu Gly His Ser
      55                60                65
CTC ARA CGG GCA GAG CGG GGA GTG GGT GGT GGG GTG TCT CCT GGG      400
Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val Ser Pro Gly
      70                75                80

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 13..87
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 4.6
 seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ATCGAATGCA GA ATG GTT TTG GGA GCC CTG AAC CTT CCC TCC CAG GAA CTC   51
      Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu
      -25                      -20                      -15

CCC ACT CTC CTG CTC CTC CCA GTG GGG GCA CCT GGR AAG AAA AAA GGC   99
Pro Thr Leu Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly
      -10                      -5                      1

ATG GAA GGC AAA ACT CCC TTG GAC CTG TTT GCT CAT TTT GGC CCT GAG   147
Met Glu Gly Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu
      5                      10                      15                      20

CCA GGG GAC CAC TCA GAT CCG CTG CCT CCC TCT GCA CCC TCT CCC ACT   195
Pro Gly Asp His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr
      25                      30                      35

CGG GAG GGG GCT CTG ACC CCG CCC CCA GGG   225
Arg Glu Gly Ala Leu Thr Pro Pro Pro Gly
      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..263
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq QTFVSFLSIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

ATACACCTCC ATTTTAAATG TGCTGCAATA TGAATGAAGT GACCTGTGTT TCATCACTTG   60
TTCAAATGAT TCTTATCCAT GTTTTGTAC TTAGTAAGGG CCATACGTAG TGGGATTAAA   120
TATTTGTGCC CTTGCTTTGA AAACAAACT GAAAGTGAAT GACACATAAG GGCAGGGATT   180
  
```

TCAGAACAGA TTTTCTTGA ATAAAA ATG CTT GTG TCA AAA ATT CAA ACA TTT 233
 Met Leu Val Ser Lys Ile Gln Thr Phe
 -15

GTC TCT TTC CTT TCC ATT CCA GTT CTA GGT CTC GTT CCA GAT CAT ATT 281
 Val Ser Phe Leu Ser Ile Pro Val Leu Gly Leu Val Pro Asp His Ile
 -10 -5 1 5

CTC CAG CTC ATA ACA GAG AAA GAA ACC 308
 Leu Gln Leu Ile Thr Glu Lys Glu Thr
 10 15

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 188..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCATAGTCA CTTTCCAAGT TTATGACCCA GAGCAATCTG ACCTGGTAG CTTGTCTCCC 60

TCATTAAATT CTCTGACTTC ATAATCAGCT CACATTCCTT TCCTCTCTTT CCCTCTCTTT 120

TTAAATATCT GTAAACATT CAAATTGATC CACGTAGATT TATCTTGCTT TTAGGCCACA 180

CTCTGAG ATG TGT AAT CCG GTT GCT CAC ACA TTT AGA GGA GTC CAT GAG 229
 Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu
 -30 -25 -20

CAT CAC GCC ATG CTA CTC TCC ACT GGT TTG AAC ATC TTA GGC ACT CAG 277
 His His Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln
 -15 -10 -5

GCA TTC CGT TAC GAA GAT GGG CAG CTG 304
 Ala Phe Arg Tyr Glu Asp Gly Gln Leu
 1 5

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 126..176
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq ILLWEACTGRCQA/SL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

TATTCAGTTG GGGGCAAGCC AGCCATGATG TGGACCTTTC ATTGGGTAGG GCAAGTCCCC   60
AAAGTTGGAA AAATGGAAAG TGGGAGCTGT GAGGCACGTG TTACACCCAC ACTTTCCTCC  120
TACAG ATG CAG TGT TGG ATT TTG TTG TGG GAG GCA TGC ACA GGT AGG TGC   170
Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys
      -15                -10                -5

CAG GCC TCC CTA CTC TCT CCC TGG CCC AGA GGT GGC AGG GGC AAG TTA   218
Gln Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu
      1                5                10

GTG GCA GTG GTG GCT GCA AAA TGG TTG GCA GCA ATC TGT GGG ATT TGG   266
Val Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp
      15                20                25                30

GCT ATC AAA GAA ATG CCA AGC CAT GGC CAC AGT CTT CAA GCA GGG GCA   314
Ala Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala
      35                40                45

GGG GAA GGT GCA CTG GTG ACC TGG AGC CTG CAA ACC TCA TTT GGT GTG   362
Gly Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val
      50                55                60

AAG CAG TAT AAG TGG GGA GTT GTG TGG CAT GAA GCA AAC CTG TTG CTT   410
Lys Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
      65                70                75

```

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 149..223
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq VLCILGCHGNLCC/EP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

ATTTTAGAAA GTAAGGAAAT AAAACTTTAA TTGAACTTGG AATAAACTCA GTTCTGAGCA   60
TTCCATTCTA CTCTGCAGTT GTCATTTATA GACAGCTGTG GATCATAATA CCTATAGACT   120
AGATATCGTT ATCTACTTAT TTATATTA ATG ACA GGA TAT CCC TGG GCA AAC   172
                        Met Thr Gly Tyr Pro Trp Ala Asn
                        -25                      -20

AGC ATC ACC ACT GTA CTG TGT ATT CTT GGT TGT CAT GGG AAC CTT TGC   220
Ser Ile Thr Thr Val Leu Cys Ile Leu Gly Cys His Gly Asn Leu Cys
   -15                      -10                      -5

TGT GAA CCA GCA GTG AGA GCA CTC GGG   247
Cys Glu Pro Ala Val Arg Ala Leu Gly
   1                      5

```

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 475..546
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq IFTALFLXLHSA/IN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATTTATGGA TGCCTACCAT CTACCAGGTA CTGTTCTAGC TACAGGAAT AACTAAAAAT   60

```

```

AGGTAAACAA AACAGATGAA AAACCTAGAA ATTTATACTG ATGTTATCAG AGTAATGTTT 120
AATTTTTCAG ATAATTGTTA TGTCTAAATT AGCATTTGAT TTTTCAATTA AGAATTTTTA 180
AATTATCCAA TATTGCAAGC ATATATAGAA ACATGGAAAA CAACAAAATT CTCATGCATA 240
TACTTCAAAC ACAGAGCTAA CAGATGTTAT TATTTTTTAT TTCTTTCACA ACCCAACTTT 300
CGGGAAACAA AATAGGCACA GCAAACTGG GATCTCCTCA TCCCCTTCTC CTTTCTTATA 360
TAAAAGTAAT CCTGCTCTTG GTACAGCTAT GTATCATACT CATCCAGGTT TTAATTTTTC 420
TTATATAACG GAACATATAT GGTGTTATTT TACGGATTTT AAAGCTTTAC ATAA ATG 477
                                         Met
GTG TCA TGT GAT GTW CVN TCT TAT GTG ATC ATT TTT ACT GCA CTC TTT 525
Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu Phe
      -20                      -15                      -10

TTA WTG CTG CAT AGT GTG GCA ATA AAT GAA GAG TTT 561
Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..139
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

ATGATAAGGG CTTATTCACA TTATTCATTC TTGAATGAAT TTTGATAGTG TCTGTCTTTC 60
AGGAACTTTG TCCTAAGTA ATG AAA TCC TTT GAT AAA AAG TTG TTT GCA ATA 112
      Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile
      -20                      -15                      -10

TTT CTT ATG TGT TTA AAG TCT ATA GGT TCT GTG GTG ATG CCC CAG CCG 160
Phe Leu Met Cys Leu Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 36..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

ATTTTCCTCC CCGCAACCTG GTGAAAGCCA AYKCA ATG TTC GGT GCG GGG GAC      53
                               Met Phe Gly Ala Gly Asp
                               -30

GAG GAC GAC ACC GAT TTC CTC TCG CCG AGC GGC GGT GCC AGA TTG GCC      101
Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser Gly Gly Ala Arg Leu Ala
-25                      -20                      -15

TCA CTT TTT GGA CTG GAT CAG GYA GCY SST GGC CAT GGA AAT GAA TTT      149
Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa Gly His Gly Asn Glu Phe
-10                      -5                      1                      5

TTC CAG TAC ACA GCC CCA AAA CAG CCT AAG AAA GGC CAG GGA ACG GCA      197
Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys Lys Gly Gln Gly Thr Ala
10                      15                      20

GCA ACA GGA AAT CAG GCA RCA CCA AAA ACA GCA CCA GCC RSC ATG AGC      245
Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr Ala Pro Ala Xaa Met Ser
25                      30                      35

ACT CCC ACA ATA CTG GTC GCA ACA GCA GTC CAT GCA TAT CGA TAC ACA      293
Thr Pro Thr Ile Leu Val Ala Thr Ala Val His Ala Tyr Arg Tyr Thr
40                      45                      50

RAT GGT CRA TAT GTA AAG CAG GSR AAT TTG GTG CTG CAG TTC TGG      338
Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu Val Leu Gln Phe Trp
55                      60                      65

```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 107..190

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.5

seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

AAAGTCAGCG CTGGAGTCGG CTAGGCGGCT GGAAACGGCG GCTGCCGCCG GTGACTCAGG      60
GAGGCGGGAG GCCGMSGGMG GAGCTCTTCC TGCAGGCGTG GARACC ATG GTG CTC      115
                               Met Val Leu
ACG CTC GGA GAA AGT TGG CCG GTA TTG GTG GGG AGG AGG TTT CTC AGT      163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25                -20                -15                -10
CTG TCC GCA GCC GAC GGC ASC GAT GSC AGC CAM GAC AGC TGG GAC GTG      211
Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser Trp Asp Val
                -5                1                5
GAG CGC GTC GCC GAG TGG CCC TGG CTC TCC GGG ACC ATT CGA GCT GTT      259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
                10                15                20
TCC CAC ACC GAC GTT ACC AAG AAG GAT CTG AAG      292
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
                25                30

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 361..411

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

ATGAAAACAG TTTTCTTTGT GATTGTGCAA TTGATGTTTA AACAGTGTTT ATCCTTCCAG   60
GTAGTATGAT GATGTATTTG TTGGAGACAA ARTATTTGCC CTAGCCTTTT TACTAATATT  120
TCAGATGAGA TTCTGTGGAG GAGAAGCATC TCCCCAAATG TCCTTGTTTT ATAGTAAATA  180
ATTCTACCAC GAGGATCCTT ATCCATAAAT CTATATTCAT GTTTATTTTG TGCTAGATAC  240
AGATCTTGCA ATATTCATGA AGCTTTAAGA AGAGCACTTT GAATCTTAAA AGAGATTCTC  300
TGAGCAGGGG TTGGCAGTGG TGAGGTCCAG GTAGTTATAA TAGCCATAAG AGCAGGGATT  360
ATG GTT ATT GAG CTC ACC AGT GTG TTT CAA GCC ATG ATC TGG AGT CAA   408
Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
      -15                      -10                      -5

GGT GTT AGT GAT TCC TCT AAG                                     429
Gly Val Ser Asp Ser Ser Lys
      1                      5
  
```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

ATDCGGCCCT GGAGCAAGCC GGGGCCTGST CGGCARCTGG GCCGCC ATG GAG TCC   55
                                   Met Glu Ser
                                   -50

ACG CTG GGC GCG GGC ATC GTG ATA GCC GAG GCG CTA CAG AAC CAG CTA  103
Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln Leu
      -45                      -40                      -35
  
```

GCC TGG CTG GAG AAC GTG TGG CTC TGG RRT SAC CTT TKC TNG SCG ATC	151
Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa Xaa Xaa Ile	
-30 -25 -20	
CCA AGK ATC CTC TTT CTG TTC TAC TTC CCC GCG GCN TAC TAC GCC TCC	199
Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr Tyr Ala Ser	
-15 -10 -5 1	
CGC CGT GTR GGC ATC GCG GTG CTC TGG ATC AGC CTS ATC ACC GAG TGG	247
Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile Thr Glu Trp	
5 10 15	
CTC	250
Leu	

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 196..270
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATNCTGTGTT ACTCATTTCC TGTCTCAGAT ACTTTGGATC CCTTGGTTCT GATCTTTCAG	60
GGGGAGAGGG CATGTTAAGA GGAGTAAGTA GATGGATGAT CTTACACAAT TGAACCTCTC	120
TTACCTCTGG CCTTGTATGC TCTTACATAG GCTGTCCCCT CTCTACATTT TCTTATTTAA	180
GGAAAAACAC AGAAC ATG ATT ATT GTC TCA GAA TTA GGA ACC CCT ACT GGT	231
Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly	
-25 -20 -15	
GTG CTC GTA GGT GTC TTT TGG TCT ACT TTT CTC TAT TGT GAA TGT GTA	279
Val Leu Val Gly Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val	
-10 -5 1	
AAG GGG CCG	288
Lys Gly Pro	
5	

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

AGCGTTTATG GCCGCGTTAA GTCTGAGTGC CGCTTTGAGT TGTGAATGA AGTGAAGTTC    60
ATTGTCAGC GTTCGGTTC ATG AAC TGG AAT GTA AGA GGC ACC AGA GGA TTC    112
           Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe
           -20                               -15

CTG CTC TGT CCC CTG GTT TGC GGC TTG CGA CGT TGG ACA TCC CCG GAT    160
Leu Leu Cys Pro Leu Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp
-10                               -5                               1                               5

TGT TGT TTA ATA GAG AAA ACT CAC CGC GGG                                190
Cys Cys Leu Ile Glu Lys Thr His Arg Gly
           10                               15

```

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq RGLLLGLAVAAAA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AAGATAGAGG CGGCAACCTC GGAAGTGGG ACGGGTGGGC CTATATAG ATG TTG AGG      57
                                     Met Leu Arg

TGC GGA GGC CGT GGG CTT TTG TTG GGC CTG GCT GTA GCC GCA GCA GCG      105
Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala Ala Ala Ala
  -15                      -10                      -5

GTA AGG
Val Arg
  1
                                     111

```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILLMIVFSIFLLL/CN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

ACCCAGAGGC AGAAAGTAAT ATTGCTTACT ATGAGTCTAT ATATCCTGGG GAATTTAAGA      60

TGCCAAAGCA GCTCATTCAC ATACAGCGTA AGTA ATG ATT CTC TTA ATG ATT GTA      115
                                     Met Ile Leu Leu Met Ile Val
                                     -10

TTT TCT ATA TTT CTC TTA TTA TGT AAC TTG ACA GAT TTT TAT CTC TTC      163
Phe Ser Ile Phe Leu Leu Leu Cys Asn Leu Thr Asp Phe Tyr Leu Phe
  -5                      1                      5

AGG AGC GAT GGG
Arg Ser Asp Gly
  10
                                     175

```

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 149..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq SLLFIFRSILISC/FS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
ACAATTTGTT TTATAAGCCT ATATTAATTG GGTTTTGACT GAATTAATTA TATAACCATT    60
TATCTCAAAA TGAAATGTTC CATAAAATTT ATTTAAWAGT ATATACTGYA TAAGTGTAA    120
ATTATGAAAT TTAGTGGTCT TATAGAGA ATG TCT TTA TTG TTT ATT TTT AGG      172
                               Met Ser Leu Leu Phe Ile Phe Arg
                               -10

TCA ATT TTG ATC TCC TGC TTT TCA GGA GAC TTT TTT TTT TTT            214
Ser Ile Leu Ile Ser Cys Phe Ser Gly Asp Phe Phe Phe
-5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 27..77
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq SKVLIQLSQAFWA/SP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ACCTGGTATG AATTACAAAA CTGTAA ATG CCT TTG ATT AGT AAA GTT TTG ATA 53
Met Pro Leu Ile Ser Lys Val Leu Ile
-15 -10

CAG CTA AGC CAA GCA TTT TGG GCC TCA CCT GAG GGT AGG AAC AGT TCT 101
Gln Leu Ser Gln Ala Phe Trp Ala Ser Pro Glu Gly Arg Asn Ser Ser
-5 1 5

GGG AGT AAG AGG AAG CAG TTG GTA GCT GCA GTG GAG ATG CGA TAC TGT 149
Gly Ser Lys Arg Lys Gln Leu Val Ala Ala Val Glu Met Arg Tyr Cys
10 15 20

AAA AGG CAG CAG GGG 164
Lys Arg Gln Gln Gly
25

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 142..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AAGTTGTAAT CCCACTAAGA ACCGCCAGGG CGAGACGAAA GCGACATCGC TTCCATCTTT 60

ACGACCAAGA ATCGCCTTCA GCCCTGTCTG GTGCATCCTT GGCAGAAAGT GAGGAGGRAA 120

ACACCCCCAT TGTTCTTTGG C ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA 171
Met Asp Thr Ser Ser Val Gly Gly Leu Glu
-25 -20

TTG ACT GAT CAG ACT CCT GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT 219
Leu Thr Asp Gln Thr Pro Val Leu Leu Gly Ser Thr Ala Met Ala Thr
-15 -10 -5

AGT CTC ACG AAT GTA GGA AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA 267
Ser Leu Thr Asn Val Gly Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu
1 5 10

GTG TCT AGA TCT AAT AAG TTT CAG AAC TCG TCA GTG GAA GAT GAT GAT 315

Val	Ser	Arg	Ser	Asn	Lys	Phe	Gln	Asn	Ser	Ser	Val	Glu	Asp	Asp	Asp		
15						20					25						
GAT	GTT	GTT	TTT	ATC	GAA	CCT	GTA	CAA	CCT	CCC	CCA	CCT	TCT	GTA	CCA	363	
Asp	Val	Val	Phe	Ile	Glu	Pro	Val	Gln	Pro	Pro	Pro	Pro	Ser	Val	Pro		
30					35				40						45		
GTG	GTA	GCT	GAT	CAA	AGA	ACC	ATA	ACA	TTT	ACA	TCA	TCA	AAA	AAT	GRA	411	
Val	Val	Ala	Asp	Gln	Arg	Thr	Ile	Thr	Phe	Thr	Ser	Ser	Lys	Asn	Xaa		
				50					55					60			
GAA	CTA	CAA	GGA	AAT	GAT	TCC	AAA	ATT	ACT	CCT	TCC	TCA	AAA	GAG	TTG	459	
Glu	Leu	Gln	Gly	Asn	Asp	Ser	Lys	Ile	Thr	Pro	Ser	Ser	Lys	Glu	Leu		
			65					70					75				
GCA	TCT															465	
Ala	Ser																

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..184
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq ILLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

ACACACGTCC	CGCMGTGGAT	ACTGGAGAAT	CCTTGCCACA	CACGTCCTGC	CGTGGACACT	60	
GGAGAATCCT	TCTCGCCACA	CACTTCCCAC	C	ATG	GAC	ACT	GGA
				Met	Asp	Thr	Gly
				-30			-25
TCG	CCA	CAC	ACG	TCC	TGC	CGT	GGA
Ser	Pro	His	Thr	Ser	Cys	Arg	Gly
			-20			-15	-10
CAC	GTC	CCA	CCG	TGG	ATA	CTG	GAG
His	Val	Pro	Pro	Trp	Ile	Leu	Glu
		-5		1			5
CCC	CTG	GAC	ACT	GGA	GAA	TCC	TTC
Ala	Val	Asp	Thr	Gly	Glu	Ser	Phe
10				15			20

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

·(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 154..246
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ATAGGACTGC	TACAAAAACC	CCATGTTTAC	GAATTTGCCA	GTGATATTGC	CCCCTTCCTG	60
GTGCATCCCA	ATTTATGGAT	ACGTTATGGT	GCCGTGGGAT	TTATCACAGT	GGTAGCTCGT	120
CAAATAAGTA	CAGCTGATGT	CTACTGTAAA	CTG ATG CCT	TAT CTT GAC	CCA TAT	174
			Met Pro Tyr	Leu Asp Pro Tyr		
			-30		-25	
ATT ACC CAA CCA	ATA ATA CAG	ATT GAA AGA	AAA CTT GTT	CTG CTC AGT		222
Ile Thr Gln Pro	Ile Ile Gln Ile	Glu Arg Lys	Leu Val Leu	Leu Ser		
	-20	-15		-10		
GTT TTA AAG GAA	CCA GTA AGT	CGT TCT ATA	TTT GAT TAT	GCT TTG AGG		270
Val Leu Lys Glu	Pro Val Ser Arg	Ser Ile Phe	Asp Tyr Ala	Leu Arg		
	-5	1	5			
TCT AAA GAT ATT	ACT AGC TTG	TTC AGA CAT	CTT CAC ATG	CGT CAG AAG		318
Ser Lys Asp Ile	Thr Ser Leu Phe	Arg His Leu His	Met Arg Gln	Lys		
	10	15	20			
AAA CGA AAT GGT	TCT CTT CCC	GAC TGC CCT	CCG CCA GAG	GAT CCT GCC		366
Lys Arg Asn Gly	Ser Leu Pro Asp	Cys Pro Pro Pro	Glu Asp Pro Ala			
	25	30	35	40		
ATA GCA CAG CTT	CTG AAG AAG	TTG CTC TCA	CAG GGA ATG	ACA GAG GAA		414
Ile Ala Gln Leu	Leu Lys Lys Leu	Leu Ser Gln Gly	Met Thr Glu	Glu		
	45	50	55			
GAG GAA GAC AAA	CTT CTG GCA	CTG AAA GAC	TTC ATG ATG			453
Glu Glu Asp Lys	Leu Leu Ala Leu	Lys Asp Phe	Met Met			
	60	65				

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 181..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

ARRAAAGCCG GGACTGGACC GAGCGGAGTK KTGCGTGTCTG CCGAAGGGGG GTKGGCCGGG   60
GGAGGKGAGG TTCGTTCCGC GGAACCGCAG YCAGAASCCK GRACCAAGAA TCGCCTTCAG   120
CCCTGTCTKG TGCATCCTTG GCAGAAAGTG RKGAKGAAAA CACCCCCATT GTTCTTTGGC   180
ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA TTG ACT GAT CAG ACT CCT   228
Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
          -25                      -20                      -15

GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT AGT CTC ACG AAT GTA GGA   276
Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
          -10                      -5                      1

AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA GTG TCT   312
Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 33..116
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq FGLLDEVVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

ATTTT	TATG	ACATCT	AWTT	ATATTG	AGTT	GC	ATG	CAT	GTT	TIG	TTC	AAC	ATA		53	
							Met	His	Val	Leu	Phe	Asn	Ile			
										-25						
GTC	ACA	ACA	AAT	WRR	RAT	AAC	CAT	TTT	GGG	TTG	TTA	GAT	TTT	GTT	GTG	101
Val	Thr	Thr	Asn	Xaa	Xaa	Asn	His	Phe	Gly	Leu	Leu	Asp	Phe	Val	Val	
	-20					-15					-10					
CAG	TGT	TGT	GAT	TCA	TTA	AGA	AAC	CAT	ARG	WGG	TCA	TTT	CAG	TCA	TCT	149
Gln	Cys	Cys	Asp	Ser	Leu	Arg	Asn	His	Xaa	Xaa	Ser	Phe	Gln	Ser	Ser	
	-3				1				5					10		
TAC	TTG	AGG	CTA	AAT	CAT	TCA	TGR	CAT	ACA	TGT						182
Tyr	Leu	Arg	Leu	Asn	His	Ser	Xaa	His	Thr	Cys						
			15					20								

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 150..215
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

ATGTATACTG AGGTTTCAGGA ACTGCTGGAG AGATGACTGG GCACCAAGAG GATGACAGTG 60
ACTCAGCTGG CATCCCTTAG CTGGTTCATG GCAGAGCTGA GTGGCCACTC CTGTCTCTGA 120
CCCCAGCTTC AGTGCTCTTT ATCTCCTCC ATG CCT CCT CAG TCG TGC TGC TCT 173
Met Pro Pro Gln Ser Cys Cys Ser
-20 -15

```

AAG ACT GCT TAC TGG CTT TCC TTC ATG TCC TGG GCA CAG AGC AGT TCT      221
Lys Thr Ala Tyr Trp Leu Ser Phe Met Ser Trp Ala Gln Ser Ser Ser
          -10                      -5                      1

TTT GGT AGC AGA HTT GAG TCC ACT TCC CCC TGC ACA GAT CAC TGC TCA      269
Phe Gly Ser Arg Xaa Glu Ser Thr Ser Pro Cys Thr Asp His Cys Ser
          5                      10                      15

GGA CCC AGA GAG GAG CAG CTC TGC TCC AGC AGG GTT TTC CAT TGC ATC      317
Gly Pro Arg Glu Glu Gln Leu Cys Ser Ser Arg Val Phe His Cys Ile
          20                      25                      30

ACA CAC CCA AAC GGT AGG ATC CAC CGG TGG                                347
Thr His Pro Asn Gly Arg Ile His Arg Trp
          35                      40

```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 53..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

AACTTTCTTC AAGGCGGTTT GGGATTGTC TCCGCTGGCC GCTGTGCTGG TG ATG TCC      58
                                         Met Ser

TGT GTT TTC TTT CAC TTT CTT CAA GGC GGT TTG GGA TTT GGC TCC GCT      106
Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly Ser Ala
          -10                      -5                      1

GGC CGC TGT GCT GGT GAC AGG                                127
Gly Arg Cys Ala Gly Asp Arg
          5                      10

```

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 156..215
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```

AAACTCGAAC TTGGTCGGGG CGCGGATCCC GAGAGGGAAA GTCATAACAA CCGCACCAGG   60
GAGTTCGACT GGCGAACTGG AAGGCCACGC CTCCTCCCGC CTGCCCCCTC AGCCCTGTGG   120
CTGGGGGCAG AGCTCAGACT GTCTTCTGAA GATTG ATG TCT ATT TCC TTG AGC       173
                               Met Ser Ile Ser Leu Ser
                               -20                               -15

TCT TTA ATT TTG TTG CCA ATT TGG ATA AAC ATG GCA CAA ATC CAG CAG       221
Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn Met Ala Gln Ile Gln Gln
                               -10                               -5                               1

GGA GGT CCA GAT GAA AAA GAA AAG ACT ACC GCA CTG AAA GAT TTA TTA       269
Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr Ala Leu Lys Asp Leu Leu
                               5                               10                               15

TCT AGG ATA GAT TTG GAT GAA CTA ATG AAA AAA GAT GAA CCG CCA GGG       317
Ser Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Gly
                               20                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 50..151
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq SFCNAVVLSPVFQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

AAGTTATACA GAAGACTTGT AGGAAGGATG GACAAACGTT CTTAAGCCC ATG ACG GCC   58
                                   Met Thr Ala

CTT AAC CTG GTC GCT CCC TTT TCT GAT GGA GAC TCA GGC AGC GTC TCT   106
Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly Ser Val Ser
-30                               -25                               -20

CTA GCT TCT TTC TGC AAT GCT GTA GTA CTC TCT CCA GTA TTT CAG GAG   154
Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val Phe Gln Glu
-15                               -10                               -5                               1

GAG GAG CAT TTG CTA TTT CAA AAA CGA AAA ACA AAA ACC TGG CCA CCC   202
Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr Trp Pro Pro
                               5                               10                               15

AGG
Arg
205

```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

AATATGTAAC CAAAAATAAA GTGTTTCART AGTTTATGCC TCTTTCATAT AATGGTCTAG   60

AGAGAGTGTC ATTGGGGCAA AGGGCAAAGA TACAGAGGAT CTGTTTCCCT TCTATCTTGT   120

TTTTCTGTAA TCACCTAGAG CAGTGCTACT CAA ATG TGG TCC AGA CCA GTG CAG   174
                                   Met Trp Ser Arg Pro Val Gln
                                   -15

GTC TTG GGA CTT CTT GCC ACT TGT CAG CAT GCT CCC TCT CCC TCC TTT   222
Val Leu Gly Leu Leu Ala Thr Cys Gln His Ala Pro Ser Pro Ser Phe
-10                               -5                               1                               5

AAA GGT GAG ACA TGT ACA GAA ATT GAG AGT GTT TAT CTG GCC CCC ATG   270

```

Lys Gly Glu Thr Cys Thr Glu Ile Glu Ser Val Tyr Leu Ala Pro Met
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TACTGTGGTA AGCACTTAGT AATGCAAAGT ATTGTTATTC TAATTATTTT CAATAAGAAAT 60
 AGTGCCTTTT ATTGGGGAAA GAGTCTACTT GGCTGATCAC AACAAGAGGT TTATTTCTTC 120
 CTCC ATG AGG TAC CGG TTA AGG ATT CAA ATC ACA ACA TCC CTC AAT CAG 169
 Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln
 -20 -15 -10
 ATC CTG CTA TTC TTA CTG ATA AGT TGT AGG ACC TTG AGC 208
 Ile Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
 -5

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 271..345

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATGTAATGGA AGCAATCATT TTGAAAAGAG TTAAAGTTTT TTGGTAAGTC AAATAAGGAT   60
CAATGCTGCT GAAAGCTGGG ACAACACACG GGCCCTGACC AAATTGGGGT TTCTTTGTCT  120
ACCTCATACC TTCCAAATCA AAAAATAATT TCCCTAGTAT TTAAATTACT CCCCCAAATC  180
AGGAATAACT TCCTCACTGT GCTGATTTTG GTTCTTTTAA AATAAGGTGG TAATTTGAAG  240
GTAATAGTTA AACCAGTCAT AGATTATTCT ATG CCA TTC TTT TCA AAT CAG CCC   294
                               Met Pro Phe Phe Ser Asn Gln Pro
                               -25                               -20

ACT CAG GTG TCA GTC CTA CTT TTC TTT TGT TGT AGT CCT CTT TAT TCT   342
Thr Gln Val Ser Val Leu Leu Phe Phe Cys Cys Ser Pro Leu Tyr Ser
      -15                               -10                               -5

CCT TTG TTT CTG CTC CAV CTC ATC CCC CAC CAG   375
Pro Leu Phe Leu Leu Xaa Leu Ile Pro His Gln
      1                               5                               10
  
```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 32..163
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCTGCGGCCC GGCCCGGCGG GTAAATAACA G ATG CGG GTG AAA GAT CCA ACT   52
                               Met Arg Val Lys Asp Pro Thr
                               -40

AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT ACT GTA CCT   100
Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro Thr Val Pro
      -35                               -30                               -25
  
```

CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA ACT TGC CAA	148
His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu Thr Cys Gln	
-20 -15 -10	
CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA GCA ATA GCT	196
His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg Ala Ile Ala	
-5 1 5 10	
GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA AGA AGA TTC	244
Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu Arg Arg Phe	
15 20 25	
TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG TGC CTC AAG	292
Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu Cys Leu Lys	
30 35 40	
TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA CAT TCA TTG	340
Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln His Ser Leu	
45 50 55	
AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CTC AGG	376
Lys His Phe Lys Ser Ser Arg Thr Glu Pro Leu Arg	
60 65 70	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPCLQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ACTTTAAT ATG GTG TCC TTG GGT TAT TAT TTA ATA TTT GTC CTA TAT CTT	50
Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu	
-40 -35	
TGG CTT TGT TTC ATG CAA ATT AGT GAA GAG AAG TTA ATA GAG GAA CAC	98
Trp Leu Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His	
-30 -25 -20 -15	
ACA GGT ACA TAT TTA ACC TCC AGT TCA CCC CTC TGC CAG CTC CAG CCC	146
Thr Gly Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro	

-10

-5

1

CCA GGG
Pro Gly

152

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ATATTATTAA ACTTTTATT TTGAGGTTAG TGTGGATTGA AATACACTTC CAACAATTAA      60
CACAAAGGTC CCCTGTGTCC TTTACCCAGT TTTCCACAAT GGTAACATCT TACAAAAC TG      120
GAGTACA ATG TCA CTC ACA TCC AGG RTA MYA ATW ATG GWT ACA ATC AAG      169
      Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys
      -35                      -30                      -25
ATA CAG AAT ATT TCT ATT ACA AAG GTC TTG TGT TGC CTT CTT ATA GCA      217
Ile Gln Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala
      -20                      -15                      -10
ACA CCT ACT TTC TTC CTA CTC CTT CCC TCA TCC ATT CCA CGG      259
Thr Pro Thr Phe Phe Leu Leu Pro Ser Ser Ile Pro Arg
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

AAGCGCAACC GGAAGTAGCC TTCTGGGGGC CGGCTTCCTT TATCTCTGGC GGCCTTGTAG   60
TCGTCTCCGA GACTCCCCAC CCCTCCTTCC CTCTTGACCC CCTAGGTTTG ATTGCCCTTT   120
CCCCGAAACA ACTATC ATG ARC GCC GAG GCT GCC GGT GTT GTC TCC ACC TCG   172
          Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser
                    -15                      -10

GTG GCC GCG GCT GTT GCT GCT GTC GCT GCT CCT GCT GGG GCC GGG       217
Val Ala Ala Ala Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
    -5              1              5
  
```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 101..145
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

TTGGTATCTG GAGTGTGTA GTGTGTTTGT ATTTGCTTAT AAATAAGTAT TATAGATAAA   60
GATAAACTTC ATAAAGAGTG GATATTTTGG GGAAAATTTT ATG TGG ATA ATG TCA   115
          Met Trp Ile Met Ser
                    -15

TCC TGT CTG GCA TTG ACA TAC ACA AAT TCA ATC TCA CAT AGT CTT TGC   163
Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile Ser His Ser Leu Cys
    -10              -5              1              5
  
```

CTT GAG AGA GCG TAC AGT CTA TTC AAA GTT GAC
 Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
 10 15

196

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 65..124
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

ACAGTGTGGC TCGGTTGAAT AGGAGAGCTT TAACTGCATT CTCTTGTGAG AATGCAGTBG 60
 AAGA ATG CCA AGA GGA GTG TAC AAT TCA AAT GCG TTA GTG CTT GTA ACA 109
 Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr
 -20 -15 -10
 CGT GGT TCC AGT TCT CTC CCT CTT GGC TTG TAT GGT ATA AAT TGT GTA 157
 Arg Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val
 -5 1 5 10
 CAG GTA ATT AAG TTA TTT TAT AGA GGC CAT CTC CAC TGG GAA ACT TTG 205
 Gln Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu
 15 20 25
 CTG CCA TCG 214
 Leu Pro Ser
 30

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 210..341
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AATTTATGAT AGGAAATGAT TGATCAAGTG TCACACAGCT GATTATCAGG TCTCAGTCTA   60
ATATTTATTC CTTATTGGTC TCTGCTTAAC TTCAAGTAGG TTATAGATTC CTTAATGGAC  120
TGATAGTTTA TGTCTTATAG CTTTACCTTT CAGGCGCTTA GTTTCATATT GGAACATGA   180
CAAGTGAATA ATAAATACAT GATAGCTCT ATG ATT GAA CCC TGT GAG AAA ATG   233
                               Met Ile Glu Pro Cys Glu Lys Met
                               -40
AAG CAT TAT GAT ATG AAT TGG TTT CTG TGT ATG TAT GAG TGT TTT TTT   281
Lys His Tyr Asp Met Asn Trp Phe Leu Cys Met Tyr Glu Cys Phe Phe
-35                               -30                               -25
TTY CAT CTT TTG GAA ACA GAA TTT CTG CTC CCC TGT GTA CAC CCT TTC   329
Phe His Leu Leu Glu Thr Glu Phe Leu Leu Pro Cys Val His Pro Phe
-20                               -15                               -10                               -5
TCT GTA ATT GCA GTG TAT CTT TTT                                     353
Ser Val Ile Ala Val Tyr Val Phe
1

```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 134..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGCCTCCGCC TTTGCCTTCG CAGCCGCCTC CAGGGCAATT TGCATATTTC TCCAAAGAAC    60
CATCCAGAAC CTGAGCAGCC TGTCTTCAGA CAGAGATAGG CCCACGGCTG TTTCTTGAAA    120
TCTGGCGCTG GGA ATG GCC ATG TGG AAC AGG CCA TGC CAG ARG CTG CCT    169
          Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro
          -55                -50                -45

CAG CAG CCT CTG GTA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG    217
Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu
          -40                -35                -30

CCC ACG GGC CGG GAG CTG ACT GAG GCC AAC CGC TTC GCC TAT GCT GCC    265
Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala
          -25                -20                -15

CTC TGT GGC ATC TCC CTG TCC CAG TKA TTT CCT GAA CCG GGG    307
Leu Cys Gly Ile Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
          -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

ATTGTCAAAA AGACATCAA CTCAACTTCT GGGAAGACAG ATTTTAAATA CACATACTTG    60
GCTAATACTC ACAAACATAT CTAAAGTTTT GGCAAAATTA TGAGGGTGAT GGGTKGGTAC    120
TAACCTGGC ATG GAG CAG GTG TGT CTT TTG GTT TCT TAT GCA GTT GAC TCT    171
          Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser
          -15                -10                -5

GCT GCA GGG AGA TTC GGG    189
Ala Ala Gly Arg Phe Gly
          1

```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

ACAAAGAGGC AGCTCCGGA ATG AGA AAG ATA AGC CAC TGC CTC CAC TGC TGG      52
      Met Arg Lys Ile Ser His Cys Leu His Cys Trp
                -25                      -20

CCC GAG TCG GGG GCA ACA TTG AGG TGC TGG GCT TCA ACA CCC GTC AGC      100
Pro Glu Ser Gly Ala Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser
      -15                      -10                      -5

GGA AGG CTT TCC TCA ATG GCT GTK RWG SSG CKG GGG GAA AKG CCA CCA      148
Gly Arg Leu Ser Ser Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro
      1                      5                      10                      15

CAG GAT GCC TTC ACC ACA CAG TGG CTG GTG CGG GAC CTG AGG GGC AAG      196
Gln Asp Ala Phe Thr Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys
                20                      25                      30

ACT GAG AAG GAG TTT AAG GCC TAT GTG TCT TTG TTC ATG CGC CAT CTG      244
Thr Glu Lys Glu Phe Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu
      35                      40                      45

TGT GAG CCT GGG GCA GAC GGC TCT GAA ACC TTT GCC GAT GGG GTC CCT      292
Cys Glu Pro Gly Ala Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro
      50                      55                      60

CGG GAG GGA CTG AGT CGC CAG CAG GTG TTG ACC CGC ATT GGA GTC ATG      340
Arg Glu Gly Leu Ser Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met
      65                      70                      75

TCT CTC GTC AAA AAG AAG GGG CAG      364
Ser Leu Val Lys Lys Lys Gly Gln
      80                      85

```

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Heart
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 172..237
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

AAAATTTTTT TAGCCTCTAA CATGAAAGGG TCTCTTCATT GTTCTCATT GTCTTACCCG      60
CCATCCAGTG TTAAGCAGTA TGTTAAAGAG CTTCTTCTTT ACAACTTTTC CCCTCACATT      120
ATTTTYCTAC ATGCAGCAAC TTCTTTAACC AAGTTGTTTG ATTAGGAGTA A ATG TGC      177
                                     Met Cys
ATA AAC GAT CAT ATT ATT AAG CTT CTG CAC CCA TGT GGC AGC ATC ACT      225
Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser Ile Thr
-20                      -15                      -10                      -5
TTA ACT TCT TCC TCA ACC ACA CGG
Leu Thr Ser Ser Ser Thr Thr Arg
1

```

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 135..185
 - (C) IDENTIFICATION METHOD: Von Heijne matrix

CAT TGT GAG AGA TTC CTG AAA CAG CAG CAA ACT TCC ATA AAA TCT TCT	210
His Cys Glu Arg Phe Leu Lys Gln Gln Gln Thr Ser Ile Lys Ser Ser	
-65 -60 -55	
CTT CTC TGC CTG CAA GGG AAT TAT GCT GGC CAT GAC TGG TTT GTA TCT	258
Leu Leu Cys Leu Gln Gly Asn Tyr Ala Gly His Asp Trp Phe Val Ser	
-50 -45 -40	
TCT CTG TTC ATG ATA ATG TTG GGA GAC AAA GAA AAA ACA TTC CAA TTT	306
Ser Leu Phe Met Ile Met Leu Gly Asp Lys Glu Lys Thr Phe Gln Phe	
-35 -30 -25	
CTT CAT CAA TTC TCC AGG CTT CTG ACT TCT GCT TTT CTT TGG TTG CCA	354
Leu His Gln Phe Ser Arg Leu Leu Thr Ser Ala Phe Leu Trp Leu Pro	
-20 -15 -10 -5	
AGG CTA CAT ATT TCT GTA AGA CTT CAA TCT GTT TTT AAA GGA GGG TTT	402
Arg Leu His Ile Ser Val Arg Leu Gln Ser Val Phe Lys Gly Gly Phe	
1 5 10	
GAM ATT TTA AGA ACA TTA TAC TTA CAT TCA MCG GGA CGG	441
Xaa Ile Leu Arg Thr Leu Tyr Leu His Ser Xaa Gly Arg	
15 20 25	

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..219
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFVVVLFSAAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AACAGAGCCA CAGAATGCTG AGCAGTCAAC AGCATTCTT GTTCCAAGAT CACCCCTCTG	60
ACTACCTCTC TGGCTGCCAA ATTGCCAGGG CCTTCACAGT TTGATTCCAT TTCTCAGCTC	120
CAGCATTAG GTAAACCCAC CAAGCAATCC TAGCCTGTG ATG GCG TTT GAC GTC	174
Met Ala Phe Asp Val	
-20	
ACC TGC TTC TTT TGG GTG GTG CTG TTT TCT GCC GGC TGT AAA GTC ATC	222

```

Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala Gly Cys Lys Val Ile
-15                      -10                      -5                      1
ACC TCC TGG GAT CAG ATG TGC ATT GAG AAA GAA GCC ACA                261
Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu Ala Thr
                    5                      10

```

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPFWTHA/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

AAAAACGCCT TGAGGATAAG GAAGGAGAAT CAGCAAGTCC CGAGTTCCTA CGGTGTGTCA    60
GCATCGTGCT CCCACTCCCG GGAGAGAGGC ATTATCTTCA GTTTACAAAA GGGGAAAACA    120
GGTCTGGGGT TTCCAGAGTC CGCGGTTTTG CTAAGAAGCC GCAGTG ATG TTG ACG      175
                                   Met Leu Thr
                                   -20
CGG CTG GTC CTC AGT GCA CAC CTG AGT AGC ACG ACC TCT CCG CCC TGG      223
Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser Pro Pro Trp
          -15                      -10                      -5
ACG CAC GCT GCC ATC AGC TGG GAG CTG GAC AAC GTG CTG ATG CCT AGT      271
Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu Met Pro Ser
          1                      5                      10
CCC AGA ATC TGG CCC CTG
Pro Arg Ile Trp Pro Leu
          15

```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 326..445
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEFVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

ATAAACTTA GGGGAAGAT TTGCCTCTCA CTTTTTTTCT TGGAAAATGT GGGCAGCAAT   60
TTTAAAGAGA ACATGAAAAT GGAGTAGGTT GAAACCAACA TTCAGAACTT CCTTTCATGG  120
ATTGAACTT AAAGCTGAGG GAGGKTTTRA GGGTGGARKT RAGGAAGGGC TAGAAGATAG  180
CAAATTCAG AGTCATATCA GAGAATATGA ACTGTCAGTG TTTCCAATGT TTCTCTTGGC  240
TCTGCACAGC ACTTCCAAGC CCTTTTGCTC ACTGTTTTTG TTCTGCCACA CCTAGGAGAA  300
GATTCAGAGC TTGCTGAGGC AAAAC ATG CGA TAT TTC CAA GGG CCT TCC CCC   352
                        Met Arg Tyr Phe Gln Gly Pro Ser Pro
                        -40                        -35

TAT TCT GAA ATA GAA ATT GAG CTT TGT GAT CAT GTG TAT TCA TTC CAA   400
Tyr Ser Glu Ile Glu Ile Glu Leu Cys Asp His Val Tyr Ser Phe Gln
  -30                        -25                        -20

GGT CTA TGT GTT AAC CTT TTG CTA GGA TTT GAA CCT GTT ATT AGT AGG   448
Gly Leu Cys Val Asn Leu Leu Leu Gly Phe Glu Pro Val Ile Ser Arg
 -15                        -10                        -5                        1

AGC CGR MGC AGT TCA CTT GCT GTT GAG TCT                               478
Ser Arg Xaa Ser Ser Leu Ala Val Glu Ser
      5                        10

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..170
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

ACTGCAGATA CGATCCCCGC TTCAACACCT GGATACACCT GGCCAGS ATG AAN HAG      56
                                     Met Xaa Xaa
                                     -40

AAG CGC ACG CAC TKV VNS STG AGC GTG TTC AAC GGG CTC GTG TAC GCC      104
Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu Val Tyr Ala
          -35                      -30                      -25

GCG GGC GGC CGC AAC GCA GAA GGA AGC CTG GCC TCG CTG GAG TGC TAC      152
Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu Glu Cys Tyr
          -20                      -15                      -10

GTG CCC TCC ACC AAT CAG TGG CAG CCG AAG HHN SCC CTG GAG GTG GCG      200
Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu Glu Val Ala
          -5                      1                      5                      10

CGC TGC TGC CAC GCT AGC GCG GTC GCC GAC GGC CGC GTG CTG GTG ACC      248
Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val Leu Val Thr
          15                      20                      25

GGA GGC TTG
Gly Gly Leu
                                     257
  
```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 249..362
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:


```

ACATCCAGCT CTGGTAGTTT AGGCTCAATC TTACGGTGTA ATTATACAGA ATAATTAGAG   60
GCAGCTGTAT CCTTGTTTCT GATTTTAAAA TCTGRATGTT TCTYCAATTC TTTGTGTACT  120
CTCCCTTCAT TTGGTACATA TAGAAGTCTT CTTATGTGTT ATTAAAGTCT TCTAAGATAG  180
TATTCTGGTC ATTGGAGACA CCAAAAATCT ATGGGCACAG TCCTGTTCTT GTTTCTTTTG  240
CCAATAGA ATG TTC CTT AAG GTT CAG TCA CAG TCC TTT TAC DTC CCT TAC   290
      Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr
            -35                      -30                      -25

AGA GAT TGT TTA AAT TTC CAC AAA AGC ACG TAT TTA CTC TTC TTT CAC   338
Arg Asp Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His
            -20                      -15                      -10

TTG TTA CTA AAT GAC TTC TTC ACA TTT TAC NTT GCT AAA               377
Leu Leu Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
            -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..199
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

CAGAAATGTTT TTTGCTGCCT CGCTTACATG GCAAAACTCA CAAACCACCT ATACAATCCA   60
AAAGAGGGGGA AACAGCTCAT CTCATATTAA TTATGGTCCA TTTCBATGAT AGGATATT   118
ATG CAA CCA TTA AAA ATC ATA TTT TAT CTG AGT GTT AGT ATA TGG ATT   166
Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
      -25                      -20                      -15

ATT TTA ATT ATT TAT ACT TTT CAG TGT AAT TCT TCT CTG AGC ATA CTA   214
Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
      -10                      -5                      1                      5

CTT TTC GAG TTA               226
Leu Leu Glu Leu

```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..66
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AAGTGATGG ATG ATG AGA ACG ACA GCG AGA GTC GCT GCG TGT ACT GCT GCA   51
      Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala
                -15                      -10

GCC CCA TTG CAA GCC CAC GGT GCA GRC ATT CAG CAG GRT CCA GAC AGS   99
Ala Pro Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa
      -5                1                5                10

CTC TGS TCT RGA AGG CTC AGC AGA GRR GGR CTT TCT GCA GGG CGR CTG   147
Leu Xaa Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu
                15                20                25

CAC CAR AGC GAA ACA GAA GCT GAA CTG GAR GCC CCG GGT CGC GCG   192
His Gln Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
                30                35                40

```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 140..241
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```

AASCCCAASG TGCTGCCGTT GCCCGTACAA CTCGGACTTG CTGTTGCTCG AGCCGCGTCT   60
GCACGGGTCT CGGACCGAGC GGAGTCCMAG CCTCGGTCCC GGAGCCCACC TTCGCCTCGC   120
CCTTGCCCAG CCTGCGGTG ATG GAG GCG GCC ACC ACA CTG CAC CCA GGC CCG   172
                Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro
                -30                                -25

CGC CCG GCG CTG CCC CTC GGG GCC CGG GCC CGC TGG GCG AGT TCC TGC   220
Arg Pro Ala Leu Pro Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys
                -20                                -15                                -10

CTC CAC CCG AGT GCC CGG TCT TCG AAC CCA GCT GGG AAG AGT TCG CGG   268
Leu His Pro Ser Ala Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg
                -5                                1                                5

ACC CCT
Thr Pro
10
274

```

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 92..178
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq LCPVIFFPNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

AAGAAAGGAC ATTTTTTTTT TCTTGTAATA ACTAGGCTGG ATTYCCAAA TTGTTGACT   60
GGCCCGTGCC CCTCTTAATG CTTCTGTAAG A ATG CAA GGT GTC AGG CGA CCT   112
                Met Gln Gly Val Arg Gly Pro
                -25

GTC TCC TTT TCC TGG AGC ACA ACC ATG TTG TGT CCT GTT ATA TTC TTT   160

```

CCA TCC AAC TGT TGG AAA GAA TAT AAC AGG ACA CAG
Pro Ser Asn Cys Trp Lys Glu Tyr Asn Arg Thr Gln
-5 1 5

ACAAGTCTGT CCTCCCTAGG CTGGCAGCTC TGTCAGCACC CAGGTTGTTA GAATAGTTGT	60
TAAACAGGT CATTCTGTTG CCAAGTAATT ACGGGGCCTT GSACTCAGTA ACCTTCCCCA	120
CGAAGCAGGC CGTAGTGTGC TTACTGCTCT CCCTTGSCTT TCCATCCCCCT ACTTTG ATG	179
	Met
TKG GRR TTT TCT TTC YTT TTA CTT TTC YTT TAW TTT CYT TTT TTC CGC	227
Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe Arg	
-15 -10 -5	
CAG KCT GGG	236
Gln Xaa Gly	
1	

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 359..427
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLLEFRFSVIMA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
ACACTGTGAA ATGCAATTGT GCCTTGAATA AGAAGGTACC TAGAAGCCAA ATTAAAGTAA    60
TAATGACTTC TTATTGGCTT TGATTTTTCa TTGCAGTATA TGGGAATTGT ACAGCAGGAA   120
ATGCTTATCA TTAATTTCTG ATGTTTTTTCa AAGCACAACCT CGAAACATTT CGATCATACA   180
TACATAGCAG TAGAGATCTG TGCCCTTCAG GTACATTGWA TCTGACCATC AGTTTATATA   240
TGTCAATGAA TTTTAAGAAT ACTCATGTTCa ATAATAGTCA TCTATCCTTG CATTTTGAAA   300
CTGTTCTAAT CTTAGTGAAC TTGAATTGGA TTTCTGGGTCa AAAGAATGTG TTTCTTTT    358
ATG TTG CTT CTG TCC GAA GCC TTG TCA GAA TCT GTC AGA CTC TTG TTT    406
Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
      -20                      -15                      -10

AGG TTT AGT GTG ATC ATG GCG TCA GAG AAG CAA AGC TTT CAA ATA    451
Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
      -5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 319..369
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

ATTCTTCTCT GGTACCTCT ATCTACCCCC GAGTCAACAA GCCCTGCCTG ATTACGCAGC   60
AGCAGTTTCT CCTGGAGAGT ATATGCCCTT CCCTACCAGA GTGGCTGTGC TCTGTGGACC  120
AACGGCATTG GTGCCGTGGC TGGTGTTCCT ACCATTCCAG TGGGTTGGCT GCAGAGTTAT  180
CCTTTGTGGG TGGGAGAGAG CACCAGGCCT CAGGAATCTC CCTGCTGGTC CCAGCCTCCA  240
TCTCCTCCTC CCAACCCCTG AACCTCTCCC GCAACCTGCA CCTCCCCCGA GAAGCCAGCC  300
ACAGAGGCAG AGAGCATC ATG GCT CTT ATC AGC CTG CCA TGC ACG ACA GCT   351
                Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala
                  -15                               -10

TTC CCT TTA CTG TCC AGC AAG GTT TCC CAG CTT CTC TTG CCC CTC AGC   399
Phe Pro Leu Leu Ser Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
   -5                1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..193
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```

AGTGGAGAGT CGAGCCTGGG GTCGGCGGAG ACWGCTGGTG TCTGAAGCCG CTCGCGCCCA   60
GGGTGACCCT GTTTGCAGCA CG ATG TCT GAA GAA GAG GCG GCT CAG ATC CCC   112
                Met Ser Glu Glu Glu Ala Ala Gln Ile Pro
                  -35                               -30

AGA TCC AGT GTG TGG GAG CAG GAC CAG CAG AAC GTG GTG CAG CGT GTG   160
Arg Ser Ser Val Trp Glu Gln Asp Gln Gln Asn Val Val Gln Arg Val
   -25                -20                -15

GTG GCT CTG CCC CTG GTC AGG GCC ACG TGC ACC GCG GTC TGC GAT GTT   208
Val Ala Leu Pro Leu Val Arg Ala Thr Cys Thr Ala Val Cys Asp Val
   -10                -5                1                5

TAC AST GCA GCC AAG GAC AGG CAC CCG CTG CTG GGC TCC GCC TGG   253
Iyr Ser Ala Ala Lys Asp Arg His Pro Leu Leu Gly Ser Ala Trp

```

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AAAAAAG ATG GCG GCG GCG GCG GCA GCT GGT GCG GCC TCC GGG CTG CCG	49
Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro	
-70 -65 -60	
GGT CCA GTG GCA CAA GGA TTA AAG GAA GCG TTA GTG GAT ACG CTC ACC	97
Gly Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr	
-55 -50 -45	
GGG ATC CTA TCC CCA GTA CAG GAG GTG CGG GCG GCT GCT GAA GAA CAG	145
Gly Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln	
-40 -35 -30	
ATT AAG GTG CTG GAG GTG ACG GAG GAA TTT GGT GTT CAC TTG GCA GAA	193
Ile Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu	
-25 -20 -15	
CTG ACT GTA GAT CCC CAG GGG GCA CTG GCA ATC CGT CAG CTG GCA TCA	241
Leu Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser	
-10 -5 1 5	
GTC ATC TTG AAA CAA TAT GTG GAG ACT CAC TGG TGT GCC CAA TCA GAG	289
Val Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu	
10 15 20	
AAA TTT AGG	298
Lys Phe Arg	
25	

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..464
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

GTGAATTCGC CAGCGGGAGC GCGCTCGCGG WCCGCGCGTT CTCCGCTTTC CCGGCTCCGT   60
CGCTGACGCG TCGTAGASTT GGSVWGC GGG AAGGCAACGG CAGCGGGATC GGG ATG   116
                                     Met
AAC AGC GGC GGC GGC TTC GGT TTG GGC TTA GGC TTC GGC CTC ACC CCC   164
Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr Pro
-115 -110 -105
ACG TCG GTG ATT CAG GTG ACG AAT CTG TCG TCG GCG GTG ACC AGC GAG   212
Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser Glu
-100 -95 -90 -85
CAG ATG CGG ACG CTT TTT TCC TTC CTA GGA GAA ATC GAG GAG CTG CGG   260
Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu Arg
-80 -75 -70
CTC TAC CCC CCG GAC AAC GCA CCT CTT GCT TTT TCC TCB DRA GTA TGT   308
Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val Cys
-65 -60 -55
TAT GTT AAG TTT CGT GAT CCA TCA AGT GTT GGA GTG GCC CAG CAT CTA   356
Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His Leu
-50 -45 -40
ACT AAC ACG GTT TTT ATT GAC AGA GST CTG RAT AGT TGT TCC TTG TGC   404
Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu Cys
-35 -30 -25
AGA AGG TTG GTA TCT CGC TTT KTT TGN HBT TAT TTG AAT TTC TGT CCT   452
Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys Pro
-20 -15 -10 -5
GTC TGT TAT TGC TTT AGC TTT CCT AGA GAT TGG CAA GTA GAC AGT ACT   500
Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser Thr
1 5 10
CTC   503

```


Leu

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..85
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq MIEMLIFLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ATTAACAAAG AGCAAGTTTA ACCTGAGTGG TCAACTTTTG CAGCAG ATG ATT GAR	55
Met Ile Glu	
ATG CTA ATA TTT CTA GAC TGT GTC CTG TCT TCC AAA GAT ACA ATA ACC	103
Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp Thr Ile Thr	
-10 -5 1 5	
ATG TTT GTG AAG TTC ATA CCT ATT TTT CCT TTT CCT TTG CAG TTT TAT	151
Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu Gln Phe Tyr	
10 15 20	
TTG CCC TCT TTC CTT CTT TTG GAG	175
Leu Pro Ser Phe Leu Leu Leu Glu	
25 30	

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..285
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

ACATCACAAA AATTAGGTGA CCATGGTTAT GATAATTCTT TGCCTAGT ATG CAT CCA      57
                                     Met His Pro
TTT CTA GCT GCC CAC GGA CCT GCA TTT CAC AAA GGC TAC AAG CAT AGC      105
Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr Lys His Ser
-75                               -70                               -65
ACA ATT AAC ATT GTG GAT ATT TAT CCA ATG ATG TGC CAC ATC CTG GGA      153
Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His Ile Leu Gly
-60                               -55                               -50                               -45
TTA AAA CCA CAT CCC AAT AAT GGG ACC TTT GGT CAT ACT AAG TGC TTG      201
Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr Lys Cys Leu
-40                               -35                               -30
TTA GTT GAC CAG TGG TGC ATT AAT CTC CCA GAA GCC ATC GCG ATT GTT      249
Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile Ala Ile Val
-25                               -20                               -15
ATC GGT TCA CTC TTG GTG TTA ACC ATG CTA ACA TGC CGC CGG              291
Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg Arg
-10                               -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..74
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

ATCTTAGTGT GACACATGAA CCCCTCCCCT TC ATG ATC TGG CCT ATG TCT GCC      53
                                     Met Ile Trp Pro Met Ser Ala
                                     -10

```

TCT GTA GCT ACT CTC TGG TCC TTT ACC TCT TAC ATA AGC TAC CCA AGC 101
Ser Val Ala Thr Leu Trp Ser Phe Thr Ser Tyr Ile Ser Tyr Pro Ser
-5 1 5

AGG TTT TAC TAT GAT GCT TGG
Arg Phe Tyr Tyr Asp Ala Trp
10 15

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 12..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVVEVCLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAGGGTAATG G ATG GGA ATT GAT ATT TTC TAT CCT TCA CAC ATC CCA GAC 50
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp
-30 -25 -20

TTT CAT CCT ATT CAT TTA TTC ATT TAT CTA GTG TTT GTA GAG TGC CTT 98
Phe His Pro Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu
-15 -10 -5

CTG TGT ACC AGG AAC TGR GAW AGK TTG TCC KGA TTC AAC TGT GAT AAC 146
Leu Cys Thr Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn
1 5 10

GCT CAA ATA ATC TTC ACA ACA GGC TCA TCC TCT AGT GGA GGA AAT AAA 194
Ala Gln Ile Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys
15 20 25 30

CCA TTT AAA AGT AGT TTA TGT ACA GTA CAT AGA GGC CAA GAA AGG GAA 242
Pro Phe Lys Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu
35 40 45

AGA ATA GAG TGC CAA GGG AAT GGG
Arg Ile Glu Cys Gln Gly Asn Gly
50

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 24..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AAATAGCTGA TTATGAACGT TTG ATG AAA GAA CTA AAT CAA AAG TTA ACT AAT   53
      Met Lys Glu Leu Asn Gln Lys Leu Thr Asn
      -85                                -80

AAA AAC AAC AAG ATA GAA GAT TTG GAG CAA GAA ATA AAA ATT CAA AAA   101
Lys Asn Asn Lys Ile Glu Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys
      -75                                -70                                -65

CAG AAA CAA GAA ACC CTA CAA GAA GAA ATA ACT TCA TTA CAG TCT TCA   149
Gln Lys Gln Glu Thr Leu Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser
      -60                                -55                                -50

GTA CAA GAA TAT GAA GAA AAA AAC WCC AAA ATC AAG CAA TTG CTT GTG   197
Val Gln Glu Tyr Glu Glu Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val
      -45                                -40                                -35                                -30

AAA ACC AAA AAG GAA CTG GCA GAT TCA AAG CAA GCA GAA ACT GAT CAC   245
Lys Thr Lys Lys Glu Leu Ala Asp Ser Lys Gln Ala Glu Thr Asp His
      -25                                -20                                -15

TTA ATA CTT CAA GCA TCT TTA AAA GGT GAG CTG GAG GCA AGC CAG CAG   293
Leu Ile Leu Gln Ala Ser Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln
      -10                                -5                                1

CAA GTA GAA GTC TAT AAA GTA AGG GTT TTA CTT TTT AAG ATT AAA AAA   341
Gln Val Glu Val Tyr Lys Val Arg Val Leu Leu Phe Lys Ile Lys Lys
      5                                10                                15

ATG TTT TTT CAT GTA GAA GTG AGG AAC GGG   371
Met Phe Phe His Val Glu Val Arg Asn Gly
      20                                25

```

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..371
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq RLLLCILIIVCYI/LF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ACAGTCCTAC CTTTGCTGAT GCCTACTCTA AT ATG GGA AAC ACT CTA AAG GAG      53
                               Met Gly Asn Thr Leu Lys Glu
                               -110

ATG CAG GAT GTT CAG GGA GCC TTG CAG TGT TAT ACG CGT GCC ATC CAA      101
Met Gln Asp Val Gln Gly Ala Leu Gln Cys Tyr Thr Arg Ala Ile Gln
-105                      -100                      -95

ATT AAT CCT GCA TTT GCA GAT GCA CAT AGC AAT CTG GCT TCC ATT CAT      149
Ile Asn Pro Ala Phe Ala Asp Ala His Ser Asn Leu Ala Ser Ile His
-90                      -85                      -80                      -75

AAG GAT TCA GGG AAT ATT CCA GAA GCC ATA GCT TCT TAC CGC ACG GCT      197
Lys Asp Ser Gly Asn Ile Pro Glu Ala Ile Ala Ser Tyr Arg Thr Ala
-70                      -65                      -60

CTG AAA CTT AAG CCT GAT TTT CCT GAT GCT TAT TGT AAC TTG GCT CAT      245
Leu Lys Leu Lys Pro Asp Phe Pro Asp Ala Tyr Cys Asn Leu Ala His
-55                      -50                      -45

TGC CTG CAG ATT GTC TGT GAT TGG ACA GAC TAT GAT GAG CGA ATG AAG      293
Cys Leu Gln Ile Val Cys Asp Trp Thr Asp Tyr Asp Glu Arg Met Lys
-40                      -35                      -30

AAG TTG GTC AGT ATT GTG GCT GAC CAG TTA GAG AAG AAT AGG TTG CTT      341
Lys Leu Val Ser Ile Val Ala Asp Gln Leu Glu Lys Asn Arg Leu Leu
-25                      -20                      -15

CTG TGC ATC CTC ATC ATA GTA TGC TAT ATC CTC TTT CTC ATG      383
Leu Cys Ile Leu Ile Ile Val Cys Tyr Ile Leu Phe Leu Met
-10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 203:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..208
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSIPSLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

ACATGTTGAG TACTTTTTCC TCACCTGTTT TTCCATTCCT GTTAGCCGGA GCAAAGGGC   60
CTCCAACTCC TCTTTTAGAG AGAAATGACT A ATG CTC ATA CTA GCA GAT ACC   112
                               Met Leu Ile Leu Ala Asp Thr
                               -35

AGA CGT GTC CAA GGA GGT ACC TTG GGC TTA ATT CCA GCA GTT CTC AAC   160
Arg Arg Val Gln Gly Gly Thr Leu Gly Leu Ile Pro Ala Val Leu Asn
   -30               -25               -20

AGA GTC CAC GTG GCA TAT GCT ATA CCC AGC ATA CCT AGC CTC TTC TGC   208
Arg Val His Val Ala Tyr Ala Ile Pro Ser Ile Pro Ser Leu Phe Cys
   -15               -10               -5

CAG CGC TGG                               217
Gln Arg Trp
1

```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 343..402
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6

seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

CACACAATTA ATATTAATGG ATAACTAATT GGAGTAATGA TTATTAGCTA CTGAATGCTG    60
ATAATAGAAG TCATATTTAA ATGCTTACTT AGTTACTTAA GTTAGTCAAG GACTCTGAAA    120
AAAATAAGGT TTAAAGTTAA CAGTGTGATC AGTCATTCCC AGTTATCTTC TTATTTAAGA    180
ACAAGATGGT AATGCAGTTG CCTTTGTTTA TTAAATAGA AAAAATTAAA TCAGGATAAA    240
ATGACCCAAC TACAGTGATG TATTTGGACA CACTACTTCT TATCTTTCAA TATAGACTTT    300
TATTTCTGGA TTACCATAGA TGGAAATAGT ATTACTGGAC AT ATG TTG GTA GGT      354
                                         Met Leu Val Gly
                                         -20

ATT TAC TTC TGT GTT TTT CTT TTT CCC TTA ATT TCG AAT ACT TCT AGC      402
Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser Asn Thr Ser Ser
-15                               -10                               -5

TAC AAA AAT TGT CAT AAA ACT TTG CAA CAC ACT ATA CCT CCC CAC GGG      450
Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile Pro Pro His Gly
  1               5               10               15

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..126
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

ATG TTT CTC GCT CCC TCT CTG CTG ATC ACA AAG CTG CTG ACC GGG TCA      43
Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
-40                               -35                               -30

GAA AGT CCT GAT GGA AAT CCA CCA GCG CTG GGC AGG CCC CTC CTC CTC      96
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
-25                               -20                               -15

```

```

CAG GGA GCT TGT CCT TGC CTA ATT TTT CTT CGT CCT GAT GAG AAC AAA   144
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10                      -5                      1                      5

AAA GAG GGG GRG GAG GAA AAG AAA AAC CAC AAA CTT CCT TTG AAA ACC   192
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
                      10                      15                      20

AGC TTA GGG
Ser Leu Gly
                      25

```

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 235..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AAAGGTGGCT TCAGGACCAC CTCCTGAGAG CTTCGTTGTA TTTCATGTAT ATTTCCCCAA   60
ATATATCAGC ATCTGACCCT TGGCTTCTGG GAGAAAGACA GAGGCGGAAC CCTGGCCGCC   120
CCAGAGAGAG GCAGCTGTGG GGGCAGAGAT GTAACAACCC TTTGAACCTT GACCTTGGAC   180
GCCAGGCTGT CCGGGAGCTT CTCCCACAAT GGCTGTTTTG GGGATGTGAC CTGG ATG   237
                                         Met
GAC CCA TCT GCT AGC AAA TCC TGT CTG TTT TAC CTC CAA AAA GTA TCT   285
Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val Ser
-15                      -10                      -5

GGA ATT CCA GGG CTT CTC ACC
Gly Ile Pro Gly Leu Leu Thr
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

ACGTGTCCTC AGGATTTTCC TCTTGGGCTG GACAGTTTGC TCCCCTGGAG GGT ATG      56
                                     Met

AGC CTG ACT GCT AGT GGG CCA AGA GCT GCC TGG GAG GAA AGG GTG GGG      104
Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val Gly
-45                -40                -35                -30

GGT CTC CAC ACT TGG GGT GCC AAC ATT CCT ACC GCC CCT GAT TCC CAG      152
Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser Gln
                -25                -20                -15

CGG TGG CTC TGT CTT CAG GCG TAC CTG GCA TCC TTC AGT CTT GAG AGC      200
Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu Ser
                -10                -5                1

CCC CAC AGA ATC TAC CTK GAA TCT CCT CCC ACG CTC CTT TTC CCC CCG      248
Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro Pro
      5                10                15

CCG
Pro
20

```

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCGCAGAAA ATGCTAGGTG CAAAGTTTGT CGAAAGAAAG GTGAGGATGA CAAATTGATC   60
TTGTGTGATG AGTGTAATAA AGCCTTYCCA CCTGTTTTGT CTGAGGCCGG CCCTCT ATG   119
                                     Met
AAG TAC CAG ATG GTG AGT GGC AGT GCC CAG CTT GCC AGC CCG CTA CTG   167
Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu Leu
  -20                      -15                      -10
CCA GGC GCA ACT CCC GTG GCA GGA ACT ATA CTG AAG AGT CTG CTT CTG   215
Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu Leu
  -5                      1                      5                      10
AGG ACA GTG AAG ATG ATG AGA GTG ATG   242
Arg Thr Val Lys Met Met Arg Val Met
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 229..333
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

ACATCTGATC GATAATTATG TCACCTGTAC CTGTCGCCAG CTTGTCTTGT TATGACGTTA   60
GTTTTACTGC TAGAAATATC TAGTAGATGG CTGGAAATCT GCAGGCAAAG TGCAGAGGGA   120
GTGASCCTGC GAGGAGAGGG SCTGGGCAAA GTGAMBGCCC TGGGCCGCAG AGTTCTTATC   180

```

TAAAAAATGG GAACAGTAGT GTCTTCCTAA AGGCACCATG GACTTAAA ATG AAT GGC	237
Met Asn Gly	
-35	
ACG TTT CCT GGG ACT TAT GTA TAT TTG GTT GCT TAT GGG GAC TTA CGT	285
Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly Asp Leu Arg	
-30 -25 -20	
ATA TTT GGT TGC TTT TGG GGA CTT ATG TAT ATK TGG TTG CTT TTG GGG	333
Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu Leu Leu Gly	
-15 -10 -5	
TCT NAA GGG	342
Ser Xaa Gly	
1	

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 66..157
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 152..218
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 220..279
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 64..103
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..40
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 98..130
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 34..66
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..285
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..205
 id R17226
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 50..112
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.7
 seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

GAGGCTGACT GTACGTTCTT TCTACTCTGG CACCACTCTC CAGGCTGCC ATG GGG CCC	53
Met Gly Pro	
-20	
AGC ACC CCT CTC CTC ATC TTG TTC CTT TTG TCA TGG TCG GGA CCC CTC	106
Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu	
-15 -10 -5	
CAA GGA CAG CAG CAC CAC CTT GTG GAG TAC ATG GAA CGC CGA CTA GCT	154
Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg Arg Leu Ala	
1 5 10	
GCT TTA GAG GAA CGG CTG GCC CAG TGC CAG GAC CAG AGT AGT CGG CAT	202
Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser Ser Arg His	
15 20 25 30	
GCT GCT GAG CTG CGG AAC TTC AAG AAC AAG ATG CTG CCA CTG CTG GAG	250
Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro Leu Leu Glu	
35 40 45	
GTG GCA GAG AAG GAG CGG GAG GCA CTC AGA ACT GAG GCC GRC ACC ATC	293
Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala Xaa Thr Ile	
50 55 60	
TCN NVN GGA GTG GAT CGT CTG GAG CGG GAG GTA GAC TAT CTG	349
Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr Leu	

65

70

75

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 46..232
id T39765
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..46
id T39765
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..141
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

AAAATAGGAG TCTCTGGTAC TGCAAACCCA CAGCCTGGAC TCAGAGCTCA AGTCTGAACT   60
CTACCTCCAG ACAGA ATG AAG TTC ATC TCG ACA TCT CTG CTT CTC ATG CTG   111
      Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu
      -20                               -15

CTG GTC AGC AGC CTC TCT CCA GTC CAA GGT GTT CTG GAG GTC TAT TAC   159
Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr
-10          -5              1              5

ACA AGC TTG AGG TGT AGA TGT GTC CAA GAG AGC TCA GTC TTT ATC CCT   207
Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro
      10              15              20

```

AGA CGC TTC ATT GAT CGA ATT CAA ATC TTG CCC CGT GGG AAT GGT TGT	255
Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys	
25 30 35	
CCA AGA AAA GAA ATC ATA GTC TGG AAG AAG AAC AAG TCA ATT GTG TGT	303
Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys	
40 45 50	
GTG GAC CTC AAG CAT AGG	321
Val Asp Leu Lys His Arg	
55 60	

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..186
id T07474
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 16..156
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AGTTTACGTG CCATC ATG AAT TAT CAG TAT GGT TTC AAC ATG GTC ATG TCT	51
Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser	
-45 -40	
CAT CCA CAC GCT GTC AAT GAG ATT GCA CTA AGC CTG AAC AAC AAG AAT	99
His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn	
-35 -30 -25 -20	
CCC AGA ACA AAA GCC CTT GTC TTA GAA CTG TTG GCA GCC GTT TGT CTT	147
Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu	
-15 -10 -5	
GTC AGA GGC GGG CAT GAA ATC ATT TTA TCA GCA TTT GAT AAC TTT AAA	195

Val	Arg	Gly	Gly	His	Glu	Ile	Ile	Leu	Ser	Ala	Phe	Asp	Asn	Phe	Lys	
		1					5					10				
GAG	GTT	TGT	GGA	GAA	AAA	CAG	CGC	TTT	GAG	AAG	TTG	ATG	GAA	CAT	TTC	243
Glu	Val	Cys	Gly	Glu	Lys	Gln	Arg	Phe	Glu	Lys	Leu	Met	Glu	His	Phe	
	15					20				25						
AGG	AAT	GAA	GAC	AAT	AAC	ATA	GAT	TTT	ATG	GTG	GCT	TCT	ATG	CAG	TTT	291
Arg	Asn	Glu	Asp	Asn	Asn	Ile	Asp	Phe	Met	Val	Ala	Ser	Met	Gln	Phe	
	30				35				40					45		
ATT	AAT	ATT	GTA	GTC	CAT	TCA	GTA	GAA	GAT	ATG	AAT	TTC	AGA	GTT	CAC	339
Ile	Asn	Ile	Val	Val	His	Ser	Val	Glu	Asp	Met	Asn	Phe	Arg	Val	His	
				50				55						60		
CTG	CAG	TAT	GAA	TTT	ACC	AAA	TTA	GGC	CTG	GMC	GAA	TAC	TTG	GRC	AAG	387
Leu	Gln	Tyr	Glu	Phe	Thr	Lys	Leu	Gly	Leu	Xaa	Glu	Tyr	Leu	Xaa	Lys	
			65					70					75			
CTG	AAA	CAC	ACT	GAG	AGT	GAC	AAG	CTT	CAA	GTC	CAG	ATC				426
Leu	Lys	His	Thr	Glu	Ser	Asp	Lys	Leu	Gln	Val	Gln	Ile				
		80					85					90				

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id HUM75821
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id T08488
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 261..387

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..127
 id R54273
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 205..288
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```

ATTGGTAATT TTCAGCTCAC AAATGATGAA GAAATCCATA ACGTCGGAAC TTCCTTGACC      60
TTTGGATTTG GCACATTGAC CTGCTGGATC CAGGCTGCGC TGACACTCAA GGTCAACATC      120
AASAATGAAG GACGGAGAGT TGGAATTCCA CGGGTTATTC TGTCGGCATC TATCACTCTC      180
TGTGTGGTCC TCTACTTCAT CCTC ATG GCC CAA AGC ATC CAC ATG TAT GCA      231
                        Met Ala Gln Ser Ile His Met Tyr Ala
                        -25                      -20

GCC AGG GTC CAG TGG GGC CTG GTC ATG TGC TTC CTG TCT TAT TTT GGC      279
Ala Arg Val Gln Trp Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly
                        -15                      -10                      -5

ACC TTT GCC GTG GAG TTC CGG CAT TAC CGC TAT GAG ATT GTT TGC TCT      327
Thr Phe Ala Val Glu Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser
                        1                      5                      10

GAG TAC CAG GAG AAT TTC CTA AGC TTC TCA GAA AGC CTG TCA GAA GCT      375
Glu Tyr Gln Glu Asn Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala
                        15                      20                      25

TCT GAA TAT CAG      387
Ser Glu Tyr Gln
30

```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (E) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..212
id AA081335
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 212..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..98
id H88204
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 82..121
id H88204
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 284..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..52
id W31695
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..138
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LHLFHLIRPXOG/WX

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 214:

ACTCTCTGCT	GAATCCCCAA	AGGGAGTGTG	TGTATTTCCT	CCC GTTCTTN	ATCAGAGCCC	60
CCAAAATAAG	TAGGA	ATG GGC AGT GGC	TAT TCA CAT	TCA CTA CAC	CTT TTC	111
		Met Gly Ser Gly Tyr	Ser His Ser	Leu His Leu	Phe	
		-20'		-15	-10	
CAT TTG CTA ATA	AGG CCC TGS	CAA GGT TGG	RAG GRA ATT	GTC CCT GCC		159
His Leu Leu Ile	Arg Pro Xaa	Gln Gly Trp	Xaa Xaa Ile	Val Pro Ala		
	-5		1	5		
TGC TTC TGG AGA	AAG AAG ATA	TTG ACA CCA	TCT ACG GGC	ACC ATG GAA		207
Cys Phe Trp Arg	Lys Lys Ile	Leu Thr Pro	Ser Thr Gly	Thr Met Glu		
	10	15	20			
CTG CTT CAA GTG	ACC ATT CTT	TTT CTT CTG	CCC AGT ATT	TGC AGC AGT		255
Leu Leu Gln Val	Thr Ile Leu	Phe Leu Leu	Pro Ser Ile	Cys Ser Ser		
	25	30	35			

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT 303
 Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
 40 45 50 55

ACA ACA AAA CCA TCT ATA ACA ACA CCA AAC ACG TGG 339
 Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Trp
 60 65

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..116
id AA081350
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..50
id AA046671
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 157..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGGAAATCC GGATGTCTCG GTTATGAAGT GGAGCAGTGA GTGTGAGCCT CAACATAGTT 60
 CCAGAACTCT CCATCCGGAC TAGTTATTGA GCATCTGCCT CTCATATCAC CAGTGGCCAT 120
 CTGAGGTGTT TCCCTGGCTC TGAAGGGGTA GGCACG ATG GCC AGG TGC TTC AGC 174
 Met Ala Arg Cys Phe Ser
 -15

CTG	GTG	TTG	CTT	CTC	ACT	TCC	ATC	TGG	ACC	ACG	AGG	CTC	CTG	GTC	CAA	222
Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr	Thr	Arg	Leu	Leu	Val	Gln	
-10					-5					1				5		
GGC	TCT	TTG	CGT	GCA	GAA	GAG	CTT	TCC	ATC	CAG	GTG	TCA	TGC	AGA	ATT	270
Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile	Gln	Val	Ser	Cys	Arg	Ile	
			10					15					20			
ATG	GNN	RTC	ACC	CTT	GTG	AGC	AAA	AAG	GCG	AAC	CAG	CAG	CTG	AAT	TTC	318
Met	Xaa	Xaa	Thr	Leu	Val	Ser	Lys	Lys	Ala	Asn	Gln	Gln	Leu	Asn	Phe	
			25				30					35				
ACA	GAA	NNV	NAA	GGA	GGC	CWW	WAR	GCT	GCT	GGG	ACT	AAG	TTT	GGC		363
Thr	Glu	Xaa	Xaa	Gly	Gly	Xaa	Xaa	Ala	Ala	Gly	Thr	Lys	Phe	Gly		
	40						45					50				

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 144..318
id AA045920
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 319..382
id AA045920
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 153..359
id N25870
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 220..262
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 355..397
 id N25870
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 20..176
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 143..299
 id H99323
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 212..267
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 335..390
 id H99323
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 67..262
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..196
 id AA150024
 est

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 171..269
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq MTCLSVLEFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

AATCTTGTC	GAAGTCGTCG	AAAATATTTA	CACCAGCAGC	TCCAGTTCAT	ACCAATAAAG	60
AAGATCCTGC	TACCCAAACT	AATTTGGGRW	TTATCCAWGC	ATTGKCGCT	GCCATATCAG	120
TTATTAWTGK	ATCYGAATTG	GGTGATAAGA	CATTTTTTAT	AGCAGCCATC	ATG GCA	176
					Met Ala	
ATG CGC TAT AAC CGC CTG ACC GTG CTG GCT GGT GCA ATG CTT GCC TTG						224
Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu Ala Leu						
-30		-25		-20		
GGA CTA ATG ACA TGC TTG TCA GTT TTG TTT GGC TAT GCC ACC AGT CAT						272
Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr Ser His						
-15		-10		-5	i	
CCC CAG GGC CTA TAC ATA						290
Pro Gln Gly Leu Tyr Ile						

GGG AGC CCT TTG CTC AGG CAG CTT CTC CTG CCT CTC CCT CCT TTC TCC 282
Gly Ser Pro Leu Leu Arg Gln Leu Leu Leu Pro Leu Pro Pro Phe Ser
-15 -10 -5

TTC	CCT	GCC	CCA	TCC	CCG	TGC	CCT	TCT	TGG	CCT	GTG	GCG	CTG	GGG	AGC	330
Phe	Pro	Ala	Pro	Ser	Pro	Cys	Pro	Ser	Trp	Pro	Val	Ala	Leu	Gly	Ser	
		1				5					10					
CAT	GGT	GTG	GCA	TAC	TGG	GGC	TCC	TGC	TCC	TTG	GGG	CAC				369
His	Gly	Val	Ala	Tyr	Trp	Gly	Ser	Cys	Ser	Leu	Gly	His				
15					20					25						

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..274
id C16636
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 121..360
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq RASLLPMLLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

AAAAAAGAGC	TGGTTCCCTG	GCAGGCTGGA	GGGCAGGAGC	TGGGGCCACG	CTGGTCTGGG	60
ATAGTTGGGC	AGGGAGGCTG	TCTACCTGGT	CTTCCAGAAT	GGACGGCCCT	GTGGCAGAGC	120
ATG CCA AGC AGG AGC	CCT TTC ACG TGG	TCA CAC CTC TGT	TGG AGA GCT			168
Met Pro Ser Arg Ser	Pro Phe Thr Trp	Ser His Leu Cys	Trp Arg Ala			
-80	-75	-70	-65			
GGG CGC TGT CCC	AGG TGG CGG GCA	TGC CTG TCT TCC	TCA AGT GTG	AGA		216
Gly Arg Cys Pro	Arg Trp Arg Ala	Cys Leu Ser Ser	Ser Ser Val	Arg		
	-60	-55	-50			
ATG TGC AGC CCA	GCG GCT CCT TCA	AGA TTC GGG GCA	TTG GGC ATN	TCT		264
Met Cys Ser Pro	Ala Ala Pro Ser	Arg Phe Gly Ala	Leu Gly Xaa	Ser		
	-45	-40	-35			
GCC AGG AGA TGG	CCA AGA AGG GAT	GCA GAC ACC TGG	TGT GCT CCT	CAG		312

Ala	Arg	Arg	Trp	Pro	Arg	Arg	Asp	Ala	Asp	Thr	Trp	Cys	Ala	Pro	Gln	
	-30						-25					-20				
GGG	GTA	ATG	CGG	GCA	TCG	CTG	CTG	CCT	ATG	CTG	CTA	GGA	AGC	TGG	GCA	360
Gly	Val	Met	Arg	Ala	Ser	Leu	Leu	Pro	Met	Leu	Leu	Gly	Ser	Trp	Ala	
	-15					-10					-5					
TTC	CTG	CCA	CCA	TCG	TGC	TCC	CCG	AGA	GCA							390
Phe	Leu	Pro	Pro	Ser	Cys	Ser	Pro	Arg	Ala							
1				5					10							

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 50..373
id AA147010
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 156..474
id AA142584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..229
id AA043641
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 72..275
id T18932

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 146..257
id AA123074
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 165..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LTYGIILTHGASG/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

AACGCTGTGG CGGGGCAGGC GAGGCGGTCG CTTGAGCGC GCTAGTCAGC TCCCTGAAGG    60
GAGTGACGGC GGTGGGTGC CCGCGCCAC TTTGCCTTC CCGGGAGAT GTCCTTGCT    120
TCTCAGATGT AAAKGCAC TTAAAGTTGKW ATTCAACAGT GAAA ATG AGT CAT ACA    176
                                   Met Ser His Thr
                                   -40
GAG GTT AAA TTA AAA ATA CCT TTT GGA AAT AAA TTA CTA GAT GCT GTT    224
Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu Leu Asp Ala Val
-35                               -30                               -25
TGT TTG GTA CCT AAC AAG AGC TTA ACA TAT GGA ATA ATT CTT ACA CAT    272
Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile Ile Leu Thr His
-20                               -15                               -10                               -5
GGA GCA TCA GGA GAT ATG AAT CTT CCT CAT TTG ATG TCA CTG GCA TCC    320
Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met Ser Leu Ala Ser
                                   1                               5                               10
CAT CTT GCA TCT CAT GGG TTT TTC TGC CTG AGA TTT ACC TGT AAA GGC    368
His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe Thr Cys Lys Gly
                                   15                               20                               25
CTT AAT ATT GTA CAT AGA ATT AAG GCG TAT AAA TCA GTT TTG AAT TAC    416
Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser Val Leu Asn Tyr
                                   30                               35                               40
CTG AAG ACA TCA GGM RAA TAC AAA CTT GCA GGT    449
Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
45                               50                               55

```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs.
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..180
id T31666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..126
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 88..141
id R58665
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 23..77
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 39..93
id R58665
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 157..231
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..137
id R14990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..50
id R14990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..120
id T26956

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 31..150
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LCXEFXSVASCD/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

AAAAAGGGGC GGTGCAGAGG CGGCAGGAAG ATG GAG TTG GGG AGT TGC CTG GAG      54
                        Met Glu Leu Gly Ser Cys Leu Glu
                        -40                        -35

GGC GGG AGG GAG GCG GCG GAG GAA GAG GGC GAG CCT GAG GTG AAA AAG      102
Gly Gly Arg Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys
      -30                        -25                        -20

CGG CGA CTT CTG TGT STR GAG TTT RCC TCG GTC GCA AGC TGC GAT GCC      150
Arg Arg Leu Leu Cys Xaa Glu Phe Xaa Ser Val Ala Ser Cys Asp Ala
      -15                        -10                        -5

GCA GTG GCT CAG TGC TTC CTG GCC GAK AAC GAC TGG GAG ATG GAA AGG      198
Ala Val Ala Gln Cys Phe Leu Ala Xaa Asn Asp Trp Glu Met Glu Arg
      1                        5                        10                        15

GCT CTG AAC TCC TAC TTC GAG CCT CCG GTG GAG GAG AGC GCC TTG GAA      246
Ala Leu Asn Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu
                        20                        25                        30

CGC CGA CCA DGG
Arg Arg Pro Xaa
      35

```

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 52..231
id AA099777
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 85..135
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..51
 id AA099777
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..222
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 83..167
 id HSB16C031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 80..135
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 27..82
 id HSB16C031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 145..314
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 43..212
 id AA068028
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 148..255
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

AGGCAGTGAA TTGAGACCGG AGGGAATCTG GCCCCTAGAG GCTGGTACTT GGGCCCCGAAA   60
CCCCCATCTC CGGCGGAGAG ACCGTCCGAG GTAATTGTCT GCCACGAGTG CACATTCTGA   120
AAACAGGRGR WTTTAAGKTT CCTAAAA ATG GGA AGA ACC TAC ATT GTA GAA GAG   174
                Met Gly Arg Thr Tyr Ile Val Glu Glu
                -35                               -30

ACT GTT GGC CAG TAT CTT TCA AAC ATA AAT CTC CAA GGA AAG GCT TTT   222
Thr Val Gly Gln Tyr Leu Ser Asn Ile Asn Leu Gln Gly Lys Ala Phe
    -25                -20                -15

GTC TCT GGC CTT TTA ATA GGA CAG TGT TCG TCA CAA AAG GAT TAT GTG   270
Val Ser Gly Leu Leu Ile Gly Gln Cys Ser Ser Gln Lys Asp Tyr Val

```

-10

-5

1

5

ATT CTT GCC ACT AGA ACG CCA CCC AAA GAG GAG CAA AGT GAG AAC TTG 318
 Ile Leu Ala Thr Arg Thr Pro Pro Lys Glu Glu Gln Ser Glu Asn Leu
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..207
id R16604
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..474
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 207..249
id R16604
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..440
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..214
id N99558
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 109..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGTATTTCAC ACTGAGATTG TCGGCTGCGG GSTATATCCA ATTCCCCGTC TCCTCATGAA 60

TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTTCCTAAGC AGGGCAAA ATG GGG TCT	117
Met Gly Ser	
-20	
CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG ATT CCG CTT GCA CTT	165
Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro Leu Ala Leu	
-15 -10 -5	
TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC CCG AAT GGG CAA ACT	213
Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn Gly Gln Thr	
1 5 10	
TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC GTG TGG TAT TTT GAA	261
Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp Tyr Phe Glu	
15 20 25 30	
GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA GTA ACA ACA GTT CTT	309
Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr Thr Val Leu	
35 40 45	
CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA TGT TGC CAG AGT GAA AAC	357
Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln Ser Glu Asn	
50 55 60	
TGC AGC AAA AAA TAT GTG ACA CTG CTG TCA ATT ATC TTT TCT TCC CTC	405
Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe Ser Ser Leu	
65 70 75	
GGA ATT GCT TTT TCT GGA TAC TGC CTG GTC ATC TCT GCC TTG GGT CTT	453
Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala Leu Gly Leu	
80 85 90	
GTC CAA GGG CCA TAT TGC CGC	474
Val Gln Gly Pro Tyr Cys Arg	
95 100	

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..214
id N99558

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 399..459
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 278..338
 id N99558
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 359..407
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 237..285
 id N99558
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 128..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..207
 id R16604
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 333..386
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 207..260
 id R16604
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 10..72
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AAGGGCAAA ATG GGG TCT CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG   51
  Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu
    -20                      -15                      -10

ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC   99
  Ile Pro Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe
    -5                      1                      5

CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC   147
  Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr
    10                      15                      20                      25

GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA   195

```

Val	Trp	Tyr	Phe	Glu	Gly	Ile	Cys	Phe	Ser	Gly	Ile	Met	Met	Leu	Ile		
				30					35					40			
GTA	ACA	ACA	GTT	CTT	CTG	GTA	CTG	GAG	AAT	AAT	AAC	AAC	TAT	AAA	TGT	243	
Val	Thr	Thr	Val	Leu	Leu	Val	Leu	Glu	Asn	Asn	Asn	Asn	Tyr	Lys	Cys		
			45					50					55				
TGC	CAG	AGT	GAA	AAC	TGC	AGC	AAA	AAA	TAT	GTG	ACA	CTG	CTG	TCA	ATT	291	
Cys	Gln	Ser	Glu	Asn	Cys	Ser	Lys	Lys	Tyr	Val	Thr	Leu	Leu	Ser	Ile		
		60					65					70					
ATC	TTT	TCT	TCC	CTC	GGA	ATT	GCT	TTT	TCT	GGA	TAC	TGC	CTG	GTC	ATC	339	
Ile	Phe	Ser	Ser	Leu	Gly	Ile	Ala	Phe	Ser	Gly	Tyr	Cys	Leu	Val	Ile		
	75					80					85						
TCT	GCC	TTG	GGT	CTT	GTC	CAA	GGG	CCA	TAT	TGC	CGC	ACC	CTT	GAT	GGC	387	
Ser	Ala	Leu	Gly	Leu	Val	Gln	Gly	Pro	Tyr	Cys	Arg	Thr	Leu	Asp	Gly		
	90				95				100					105			
TGG	GAG	TAT	GCT	TTT	GAA	GGC	ACT	RCT	GGA	CGT	TTC	CTT	ACA	GAT	TCT	435	
Trp	Glu	Tyr	Ala	Phe	Glu	Gly	Thr	Xaa	Gly	Arg	Phe	Leu	Thr	Asp	Ser		
			110						115					120			
AGC	ATA	TGG	ATT	CAG	TGC	CTG	GAA									459	
Ser	Ile	Trp	Ile	Gln	Cys	Leu	Glu										
			125														

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 6..344
id H09880
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 355..401
id H09880
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..369
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 41..345
id H94779
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..338
id N27248
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..278
id T74091
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 273..314
id T74091
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 346..408
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC   60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC  120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG  180
GTTTGTTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA  240
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG  300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAACCTGT TAGAA ATG TGG TGG TTT   357
                                   Met Trp Trp Phe
                                   -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT   405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA   453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
  1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 29..295
id AA041777
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..222
id HSC1QB111
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 135..281
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 56..202
 id H10738
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..133
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..53
 id H10738
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 75..277
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 6..208
 id HSC2KE111
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 89..263
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 2..176
 id W24981
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 106..228
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.4
 seq PLIFSLWCSGVLL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

AAGAGTGCGC GGRSATGGG GCTTCCAGC TCTCACAGAA CCTTCAGCAT CCCAGCTGC      60
CGGTCTTGGC ATCTCGAAG TAAGGAGAGT TTAGATGCT TCTGG ATG TTC AAT GCT      117
                                   Met Phe Asn Ala
                                   -40

AGC ACC TTT ACA GAC TGG AGC AGC TCG ATT TTC TTC GTA TTT ACT TTC      165
Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe Val Phe Thr Phe
   -35                -30                -25

AAG AGC AAG AAA AGT GCT GGG CTC CCA CTT ATT TTC TCC CTG TGG TGT      213
Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe Ser Leu Trp Cys
   -20                -15                -10

TCC GGA GTT CTG CTC CAT ATC CAC CAG AAA GCT GGC GGC CCA CGG CTT      261

```

Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly Gly Pro Arg Leu
-5 1 5 10
TGG CGC ATC CAT GGC GAG CAG
Trp Arg Ile His Gly Glu Gln
15

282

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..334
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.3
region 1..181
id HSU90144
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 90..200
id T70246
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..89
id T70246
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 50..208
id T70127
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 219..328
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 62..171
 id AA114263
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 159..218
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..60
 id AA114263
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 222..308
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.4
 seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```
GACTCTTACT GTTTCATG GTGAGAAGAC AATATTTGCT TTCTCTTTT CCTTCTTCC   60
GGATGAGAGG NTAAGCCATA ATAGAAAGAA TGGAGAATTA TTGATTGACC GTCTTTATTC 120
TGTGGGCTCT GATTCTCCAA TGGGAATACC AAGGGATGGT TTTCCATACT GGAACCCWWA 180
GGTAAAGACA CTCAAGGACA GACATTTTGT GCAGAGCATA G ATG AAA ATG GCA AGT 236
                                         Met Lys Met Ala Ser
                                         -25

TCC CTG GCT TTC CTT CTG CTC AAC TTT CAT GTC TCC CTC CTC TTG GTC   284
Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val Ser Leu Leu Leu Val
          -20                      -15                      -10

CAG CTG CTC ACT CCT TGC TCA GCT CAG TTT TCT GTG CTT GGA CCT CTG   332
Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser Val Leu Gly Pro Leu
          -5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..411
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..230
 id C15003
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..411
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..230
 id HUM407E11B
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..369
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..188
 id C15677
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 212..369
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 26..183
 id HUM169E08B
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 274..399
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.2
 seq LFLDLVCHEFCQS/DD

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACCAGGAACA TCCAGCTATT TATGATAGCA TTTGCTTCAT TATGTCAAGT TCAACAAATG   60
TTGACTTGCT GGTGAAGGTG GGGGAGGTTG TGGACAGCT CTTTGATTG GATGAGAAAC   120
TAATGTTAAG AATGGGTCAG AAATGGGGCT GCTCAGCCTC TGGACCAACC CCAGGAAGAG   180
TCTGAAGAGC AGCCAGTGTT TCGGCTTGTT CCCTGTATAC TTGAAGCTGC CAAACAAGTA   240
CGTTTGTAAA ATCCAGAATG GCTTGATGTT TAC ATG CAC ATT TTA CAA CTG CTT   294
                               Met His Ile Leu Gln Leu Leu
                               -4C

ACT ACA GTG GAT GAT GGA ATT CAA GCA ATT GTA CAT TGT CCT GAC ACT   342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr

```

AAACCGTTGC	CAAGGAGCTC	GACTCTGGGA	GCGGTCTAGA	GCCCGGGCGC	CTCCTGGGGG	60
GTGGGGAAAC	GGTTTCGTGA	GGAGAATTTG	AGTTAAAATT	ATAAGACCTA	ATT ATG	116
					Met	
AGT GAT CAA ATT AAA TTC ATT ATG GAC AGT CTC AAT AAG GAG CCC TTT						164
Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro Phe						
-40		-35		-30		
AGG AAG AAC TAT AAT TTA ATC ACG TTT GWT TCC TTG GAG CCA ATG CAA						212
Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met Gln						
-25		-20		-15		
CTA TTA CAA GTT CTC AGT GAT GTT CTG GCT GAG ATT GAC CCA AAG CAA						260
Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys Gln						

-10	-5	1	5	
CTT GTG GAT ATC AGA GAG GAG ATG CCA GAG CAG ACA GCC AAA CGA ATG				308
Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg Met				
10	15	20		
TTG AGC CTT CTT GGT ATT CTT AAG TAC AAA CCT TCA GGA AAT GCC ACA				356
Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala Thr				
25	30	35		
GAT ATG AGT ACT TTT CGT CAG GGT TTG GTG ATT GGA AGT AAA CCT GTA				404
Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro Val				
40	45	50		
ATT TAC CCA GTG CTC				419
Ile Tyr Pro Val Leu				
55				

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..151
id T34361
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 152..305
id T34361
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 131..263
id HSC16A051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..130
id HSC16A051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 267..300
id HSC16A051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 41..236
id T35252
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 236..283
id T35252
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 57..143
id H92421
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 200..273
id H92421
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 85..227

id T19059
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..270
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 228..293
id T19059
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 93..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AAGACCTGGG CGTCTGGAAT GATCTACGTG CTAAATACA CCACTCGCCA CCATTTTCTC      60
CAGCTGGGAG TGTCCACTCG CCTTCCACCA GC ATG GCA ACG TCK TEA CAG KAC      113
                               Met Ala Thr Ser Ser Gln Xaa
                               -75
CGC CAG CTG CTC AGT GAC TAC GGG CCA CCG TCC CTA GGC TAC ACC CAG      161
Arg Gln Leu Leu Ser Asp Tyr Gly Pro Pro Ser Leu Gly Tyr Thr Gln
   -70                      -65                      -60
GGA ACT GGG AAC AGC CAR RTG CCC CAA AGC AAA TAC GCG GAG CTG CTG      209
Gly Thr Gly Asn Ser Gln Xaa Pro Gln Ser Lys Tyr Ala Glu Leu Leu
   -55                      -50                      -45
GCC ATC ATT GRA GAG CTG GGG AAG GAG ATC AGA CCC ATG TAC GCA GGG      257
Ala Ile Ile Xaa Glu Leu Gly Lys Glu Ile Arg Pro Met Tyr Ala Gly
   -40                      -35                      -30                      -25
AGC AAG AGT GCC ATG GAG AGG CTG AAG CGC GGC ATC ATT CAC GCT MSA      305
Ser Lys Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Xaa
               -20                      -15                      -10
GGM CTR GTT CGG GAG TGC TTG GCA GAM ACG GAA CGA ATG CCA GAT CCT      353
Gly Leu Val Arg Glu Cys Leu Ala Xaa Thr Glu Arg Met Pro Asp Pro
               -5                      1                      5
AGC TGC CTT GTT GGT TTT      371
Ser Cys Leu Val Gly Phe
    10

```

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..128
id N88564
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AACCGGCAGC TGAACCCACC CGGCGCCACG GGA	58
CTTGTGAC GCGTGCTCTG CGCTTGCC	
ATG AGA CTC CTG GGA GCT GCA GCC GTC GCG GCT CTG GGG CGC GGA AGG	106
Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg	
-15 -10 -5 1	
GCC CCC GCC TCC CTA GGC TGG CAG AGG AAG CAG GTT AAT TGG AAG GCC	154
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala	
5 10 15	
TGC CGA TGG TCT TCA TCA GGG GTG ATT CCT AAT GAA AAA ATA CGA AAT	202
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn	
20 25 30	
ATT GGA ATC TCA GCT CAC ATT GAT TCT GGG AAG	235
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys	
35 40	

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 13..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 20..169
 id N41898
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 26..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 38..174
 id H69272
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 45..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..118
 id N20619
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 13..60
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq RLLRRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

AATTGCAGGG AG ATG GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT   51
      Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser
          -15                      -10                      -5

GTC ATC TCC AGG AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC   99
Val Ile Ser Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser
          1                      5                      10

AGA GCC CTG CAG ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA   147
Arg Ala Leu Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr
          15                      20                      25

CCC AAC CCA GCG CCG GGG   165
Pro Asn Pro Ala Pro Gly
          30                      35

```

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..156
id AA069390
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 122..169
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LNSLSALAE LAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AAGGAGAGTC ACGTGAGAGT GGGCGGAGGG GGTGGAGGTT TGTCTCCGCT GTTTCATCTC   60
TATGGCTGTC AGAGGTGGGC GGCTTTGACC GAGAGGCTGC TGGAGCTCGT GTTTGGACGC   120
G ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT   169
  Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
    -15                -10                -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CTA GCC   217
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
  1                5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..169
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..126
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 170..231
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 126..187
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 230..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..216
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 129..280
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 279..340
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 172..410
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 159..299
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 182..222
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 298..338
 id T78111
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 220..254
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 337..371
 id T78111
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 89..271
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq YTAHSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GCGGCGCGGC CGTAAAGCGC CATTACGCAG AGAGAAAGTT ACGAGAACT CGTTTTTCATC	60
TTCTTGTTT CATCTTAATA CCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA	112
Met Ser Gly Ser Asn Gly Ser Lys	
-60 -55	
GAA AAT TCT CAC AAT AAG GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA	160
Glu Asn Ser His Asn Lys Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys	
-50 -45 -40	
GTT GAA CGA AGC CAG GTT CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG	208
Val Glu Arg Ser Gln Val Pro Asn Glu Lys Val Gly Trp Leu Val Glu	
-35 -30 -25	
TGG CAA GAC TAT AAG CCT GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT	256
Trp Gln Asp Tyr Lys Pro Val Glu Tyr Thr Ala Val Ser Val Leu Ala	
-20 -15 -10	
GGA CCC AGG TGG GCA GAT CCT CAG ATC AGT GAA AGT AAT TTT TCT CCC	304
Gly Pro Arg Trp Ala Asp Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro	
-5 1 5 10	
AAG TTT AAC GAA AAG GAT GGG CAT GTT GAG AGA AAG AGC AAG AAT GGC	352
Lys Phe Asn Glu Lys Asp Gly His Val Glu Arg Lys Ser Lys Asn Gly	
15 20 25	
CTG TAT	358
Leu Tyr	

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 294..347
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 297..350
 id AA038489
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 134..347
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..214
 id AA111922
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 284..331
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAAAAAGC TGCTGGACCC CAGGGAGAGC TGACCACTGC CCGAGCAGCC GGCTGAATCC   60
ACCTCCACAA TGCSGCTCTC AGGAACCCCG GYCCCTAATA AGAAGAGGAA ATCCAGCAAG   120
CTGATCATGG AACTCACTGG AGGTGGACAG GAGAGCTCAG GCTTGAACCT GGGCAAAAAG   180
ATCAGTGTCC CAAGGGATGT GATGTTGGAG GAACTGTGCG TGCTTACCAA CCGGGGCTCC   240
AAGATGTTCA AACTGSGGCA GATGAGGGTG GAGAAGTTTA TTT ATG AGA ACC ACC   295
                                   Met Arg Thr Thr
                                   -15

CTG ATG TTT TCT CTG ACA GCT CAA TGG WTC ACT TCC AGA AGT TCC TTC   343
Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser Arg Ser Ser Phe
   -10               -5               1

CAA
Gln
5

```

346

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 35..384
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 8..357
 id H11129
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 43..346
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 16..319
 id R11829
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 50..302
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..253
 id R18811
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 302..366
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 254..318
 id R18811
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 183..371
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 6..194
 id R10511
 est

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide

(B) LOCATION: 73..147
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 14.1
 seq LLLLLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```

ACTGCGCGGA TCGGCGTCCG CAGCGGGCCG CTGCTGAGCT GCCTTGAGGT GCAGTGTTCG      60
GGATCCAGAG CC ATG TCG GAC CTG CTA CTA CTG GGC CTG ATT GGG GGC CTG      111
      Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
      -25                      -20                      -15

ACT CTC TTA CTG CTG CTG ACG CTG CTG GCC TTT GCC GGG TAC TCA GGG      159
Thr Leu Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
      -10                      -5                      1

CTA CTG GCT GGG GTG GAA GTG AGT GCT GGG TCA CCC CCC ATC CGC AAC      207
Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
      5                      10                      15                      20

GTC ACT GTG GCC TAC AAG TTC CAC ATG GGG CTC TAT GGT GAG ACT GGG      255
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
      25                      30                      35

CGG CTT TTC ACT GAG AGC TGC AGC ATC TCT CCC AAG CTC CGC TCC ATC      303
Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile
      40                      45                      50

GCT GTC TAC TAT GAC AAC CCC CAC ATG GTG CCC CCT GAT AAG TGC CGA      351
Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg
      55                      60                      65

TGT GCC GTG GGC AGC ATC CTG AGT GAA GGT GAG      384
Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu
      70                      75
  
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
 region 29..172
 id T64530

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 36..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LWSLALWLPLALS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCCGGACT GATAACCAGC CGGCCAGACT GAGGG ATG GAA GGC ACT GAG ATG      53
                               Met Glu Gly Thr Glu Met
                               -30

GGG GCC CGT CCA GGC GGA CAC CCG CRG AAA TGG AGC TTT CTG TGG TCT      101
Gly Ala Arg Pro Gly Gly His Pro Xaa Lys Trp Ser Phe Leu Trp Ser
-25                      -20                      -15

CTT GCA CTC TGG CTG CCT CTT GCC CTC TCT GTG TCT CTC TTT CTT GGT      149
Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser Val Ser Leu Phe Leu Gly
-10                      -5                      1                      5

CTC TCC CTC TCT CCT CCT CAG CCT GGT CTT TCT CTT TGG TGC ACA CTT      197
Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu Ser Leu Trp Cys Thr Leu
10                      15                      20

AGT TAT TGT TGT GAG CAA TGG AAG TTC AAA GGA ACT CCC TCT CCA GCT      245
Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys Gly Thr Pro Ser Pro Ala
25                      30                      35

CTT CTG AAT CTK GGG ACA CGC GGG      269
Leu Leu Asn Leu Gly Thr Arg Gly
40                      45

```

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 207..383
id N26787
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 95..194
id N28787
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 209..305
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 97..196
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 297..382
id AA019783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 99..198
id H86396
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 300..367
id H86396
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 247..305

id H86396
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 210..326
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 108..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 98..197
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 327..368
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 318..359
id H86516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 108..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 111..210
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 272..354
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 285..367
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..286
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 223..289
id AA059290
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 139..302
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

ARCGGTTAGT GGACCGGGAC CGGTAVGGGT GCTGTWGCCA TCATGGCTGA CCCCMMCCC      60
CGGBACMCTC GCTCCTCGAT CGAGGACGAC TTCANMTMNG GCAGGCAAGC GTGGCCTCCG    120
CCACCGTGYM BNTCCGA ATG VCC TTT CTG AGA AAA GTC TMN AGC ATT CTT      170
              Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu
              -55                      -50                      -45

TCT CTG CAG GTT CTC TTA ACT ACA GTG ACT TCA ACA GTT TTT TTA TAC      218
Ser Leu Gin Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr
              -40                      -35                      -30

TTT GAG TCT GTA CGG ACA TTT GTA CMT GAG AGT CCT GCC TTA ATT TTG      266
Phe Glu Ser Val Arg Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu
              -25                      -20                      -15

CTG TTT GCC CTC GGA TCT CTG GGT TTG ATT TTT GCG TTG ATT TTA AAC      314
Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn
              -10                      -5                      1

AGV CAT AAG TAT CCC CTT AAC CTG TAC CTA CTT TTT GGA TTT ACG CTG      362
Xaa His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu
              5                      10                      15                      20

TTG GMA GCT CTG ACT GTG GCA GTT GTT GTT ACT      395
Leu Xaa Ala Leu Thr Val Ala Val Val Val Thr
              25                      30

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..155
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 24..126
id AA075942
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 66..136
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 37..107
id AA262924
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 22..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.8
seq MLLLLLLLGSQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

AAAGGGTCGT TGGTGGGAAA G ATG GCG GCG ACT CTG GGA CCC CTT GGG TCG	51
Met Ala Ala Thr Leu Gly Pro Leu Gly Ser	
-35 -30	
TGG CAG CAG TGG CGG CGA TGT TTG TCG GCT CGG GAT GGG TCC AGG ATG	99
Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met	
-25 -20 -15	
TTA CTC CTT CTT CTT TTG TTG GGG TCT GGG CAG GGG CCA CAG CAA GTC	147
Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val	
-10 -5 1	
GGG GCG GGG	156
Gly Ala Gly	
5	

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(64..95)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 79..110
id N98118
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 195..317
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 9.9
 seq ILPFLLPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

ATAGTGATCC TTTTCCTTCT CCCACTCCGT AAGTTTCTAT CCTTGGCCTC CTATTCTTTT   60
TACTACATAT ATACTTTATA TATACATATA TACTTGAAC AGGCTTAATG AGTTCCAAGG   120
TTTCAAGTAT AATAGAAGGA TAGTTTCCCT AATATTTCTT CAAACAGAT TTCTCTTCTG   180
AAATCCAGAG TCAT ATG TCC AGT TGG ATG TAT CTT GGA TAC CCC ATT GTC   230
          Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val
          -40                      -35                      -30
ACC TCA AAC ACT ACT TGT CTA AAA CTG ATC TCA TCA TCT TTT CCC CAA   278
Thr Ser Asn Thr Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln
          -25                      -20                      -15
ATC CTT CCT TTT CTT CTA TTT CCC TTC CCA GTG AAT GCC AGA TCT CAC   326
Ile Leu Pro Phe Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His
          -10                      -5                      1
TYA GTT GCT CAA ACT AAA AGC CCG AGG   353
Xaa Val Ala Gln Thr Lys Ser Pro Arg
      5                      10
  
```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 352..396
id AA021024
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 46..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.7
seq QLCLLLPSCSL/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

ACCTCTTGGG GCCTACTTTG GGATGAAGTR GCCTCCCTCA GCAGC ATG GCC CCT GGG      57
                                   Met Ala Pro Gly
                                   -20

GTC ATC ATC ATC CAG CTC TGC CTC TTG CTC CTG CCT TCC TGC TCC CTT      105
Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro Ser Cys Ser Leu
   -15                      -10                      -5

TCT GTT TCC GGA TGT TCC TGC CCT AGT GCC TGC TTC AGC ACC ACC AGC      153
Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe Ser Thr Thr Ser
   1                      5                      10                      15

CGC GAG
Arg Glu
                                           159

```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 179..213
id N78639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 193..232
id AA150442
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..377
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

ACATGCTCAG GGTGAGGTTT CAGCCCCAGC TGAGGGCTGA GGGGAGTGGG TGGACATGGG      60
GCAGGGAGCT GGAAGAACAC TCGAGAGACA GCAGGTAG ATG AGA CAT GGC TTT ATT      116
                                   Met Arg His Gly Phe Ile
                                   -90
CAG CAG CAG TTT TCA TTA ACA GCT TTC TCA MAC STT WRG SCW ATC TTC      164
Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser Xaa Xaa Xaa Xaa Ile Phe
   -85                      -80                      -75
ACA CTG KST GSC CTG TCT CAG TTG CTT AGT TCA GCA GCT CCC AAA CAC      212
Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser Ser Ala Ala Pro Lys His
   -70                      -65                      -60
ACA GCT GCA CCG ACG GCC CTC CCT TGC CTT CAG GGT CAG CAG CTT AAC      260
Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu Gln Gly Gln Gln Leu Asn
  -55                      -50                      -45                      -40
TCT CTC TCT CTG GGC ACA AGT GAG CTG AGC TGT GTC CTG GCT TCC TCC      308
Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser Cys Val Leu Ala Ser Ser
   -35                      -30                      -25
TGT CTA TCT ACA AAG ACA GAC CCC TCT GGT CTC TCT CTC TCT TTG GGT      356
Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly Leu Ser Leu Ser Leu Gly
   -20                      -15                      -10
GCC AGC GCA CCT GTA CAG TGT CAG CAG GAC AAT TAT ACC TTT TGC KNN      404
Ala Ser Ala Pro Val Gln Cys Gln Gln Asp Asn Tyr Thr Phe Cys Xaa
   -5                      1                      5
CAA TAC TGG CTT AGA GCA AGG CAT      428
Gln Tyr Trp Leu Arg Ala Arg His
  10                      15

```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 325..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 277..323
id AA015589

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 325..371
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 277..323
 id AA019963
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 140..262
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.5
 seq LIIFLSFLPFINS/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

ACAAGTGGGA TAGGTCCTGT GACAGAATTG TGTGATACAG GTCAAACAGG AGTTGGGTTA   60
TGGGGAAAT  GCCAGTTGAA ATATGTTTTG ATCTTTGGAG AAACCTATTT TTTCATTTAA  120
CCTGTTCTTT AAATCCAGT ATG  TTC CAG AAC ATA CAA AAA TGT TTA AAT GTT   172
           Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val
           -40                               -35

CCA TTT GTA AGA GGA TAT CAT GTA TTT TAT ATC AAT TTA AAT GCA GTT   220
Pro Phe Val Arg Gly Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val
-30                               -25                               -20                               -15

ATC CTA ATC ATT TTT CTT TCA TTT TTA CCC TTT ATT AAC TCT TCA TTT   268
Ile Leu Ile Ile Phe Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe
           -10                               -5                               1

GTT TAC AAA ACA AAT CCA CTC TAT GAC GCA ATC TCT AAT TAT GTG TTT   316
Val Tyr Lys Thr Asn Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe
           5                               10                               15

TCT TTC AGG TAT CCA AAC CTT GRA ASC TTT GCT CTA GAT GTC AGG CTT   364
Ser Phe Arg Tyr Pro Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu
           20                               25                               30

GTT TTT
Val Phe
35

```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (E) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(215..358)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 165..308
 id R98055
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 185..289
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 252..356
 id W23510
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 136..186
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 202..252
 id W23510
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 73..109
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 139..175
 id W23510
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 315..352
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 385..422
 id W23510
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(215..358)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 144..287
 id T46976
 est
- (ix) FEATURE:
 (A) NAME/KEY: other

(B) LOCATION: complement(227..358)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 167..298
 id AA084768
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(248..358)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 169..279
 id R50108
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(215..250)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 278..313
 id R50108
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 281..340
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.2
 seq FPLALFLSGSLA/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGAGTGAGAC GGGCAGATGG AGGAGGGATT GTAATGGCGG YAGCGGCAGC TCCSTGCTC   60
TGACCCACGG CAGGCATACA GCATCCGATT TAATCTGGAT CCATTCCGGC GCCTTCCTCT   120
CCCAGTCACC CAGAGGGCCC CAACCCCGGC GGCCCTTTCT TCCTCAAATG TCCTCGGCTC   180
TATACCGTGC CTGGGTCTTT TCTCTTTCTC TCTGCCTGGA AGATTCCTTC TTTCCCCTTT   240
TGTCTTGCCC ACTCCTGTTT ACCCTTCAAG TTTCAAGTTC ATG TCA CTG TCT CAG   295
                               Met Ser Leu Ser Gln
                               -20

AGA GGT TTT CCT GTG CTC GCC CTG TTT CTC TCA GGA AGC CTT GCT CTT   343
Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser Gly Ser Leu Ala Leu
-15                -10                -5                1

TTC CAT CAT ACC TCT GGG                               361
Phe His His Thr Ser Gly
5

```

(2) INFORMATION FOR SEQ ID NO: 244:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..132
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..114
id N87112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 174..247
id N87112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 111..176
id N87112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 68..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..200
id T68050
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..209
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..147
id AA157180
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98

region 1..130
id AA094982
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 190..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 5..79
id W00395
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..145
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ACCCACCCTC AGACCTAGCC GGAGCAAAGT TTCACTTATA GAAGGGAGAG AAGCGAAC      58
ATG GCA GCG CGT TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG      106
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
          -25                -20                -15

GCG CTG CTC ATC GTT TGC GAC GTT CCC TCA GCC TCT GCC CAA AGA AAG      154
Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
          -10                -5                  1

AAG GAG ATG GTG TTA TCT GAA AAG GTT AGT CAG CTG ATG GAA TGG ACT      202
Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
          5                10                15

AAC AAA AGA CCT GTA ATA AGA ATG AAT GGA GAC AAG TTC CGT CGC CTT      250
Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
          20                25                30                35

GTG AAA GMN CCA CCG AGG      268
Val Lys Xaa Pro Pro Arg
          40

```

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 45..241
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..38
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..208
id W01412
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..199
id AA044118
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 13..209
id W42797
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 95..213
id R39635
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 15..94

id R39635
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 191..286
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```

AACAAAGTATG TTACGATGGC TCGATTGCTT TTGCCTAGCG GAAACCATTC ACTAAGGACC   60
GAGCACCAAA TAACCAAGGA AAAGGAAGTG AGTTAAGGAG GTACTCGTCT TGGTGAGAGC   120
GTGAGCTGCT GAGATTTGGG AGTCTGCGCT AGGCCCGCTT GGAGTTCTGA GCCGATGGAA   180
GAGTTCACTC ATG TTT GCA CCC GCG GTG ATG CGT GCT TTT CGC AAG AAC       229
      Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
                -30                      -25                      -20

AAG ACT CTC GGC TAT GGA GTC CCC ATG TTG TTG CTG ATT GTT GGA GGT       277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
                -15                      -10                      -5

TCT TTT GGT CTT CGT GAG TTT TCT CNA ATC CGA TAT GAT GCT GTG AAG       325
Ser Phe Gly Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys
                1                      5                      10

GGG                                               328
Gly

```

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 104..208
id AA131932
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 298..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 293..337
id AA131932
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 67..272
id AA001989
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..102
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 11..84
id AA001989
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 76..305
id W32996
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 31..72
id W32996
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 236..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 165..306
id AA121218
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 34..163
id AA121218
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 70..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq LLVLLLYAPVGFC/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAGAGCSSCT GCGGCCGGGC GCGAAAATGG CGGCGGCGGC GACGGCCNGG CGCTCCTGAA      60
GCAGCAGTT ATG GAG CTT CCC TCA GGG CCG GGG CCG GAG CGG CTC TTT GAC      111
      Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp
                -35                      -30                      -25

TCG CAC CGG CTT CCG GGT GAC TGC TTC CTA CTG CTC GTG CTG CTG CTC      159
Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu
                -20                      -15                      -10

TAC GCG CCA GTC GGG TTC TGC CTC CTC GTC CTG SGC CTC TTT CTC GGG      207
Tyr Ala Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly
                -5                      1                      5

ATC CAC GTC TTC CTG GTC AGC TGC GCG CTG CCA GAC AGC GTC CTT CGC      255
Ile His Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg
      10                      15                      20                      25

AGA TTC GTA GTG CGG ACC ATG TGT GCG GTG CTA GGG CTC GTG GCC CGG      303
Arg Phe Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg
                30                      35                      40

CAG GAG GAC TCC GGA CTC CGG GAT CAC AGT GTC AGG GTC CTC ATT TCC      351
Gln Glu Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser
                45                      50                      55

AAC CAT GTG ACA CCT TTC GAC CAC CAG      378
Asn His Val Thr Pro Phe Asp His Gln
      60                      65

```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..181
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 1..144
id W60505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 186..312
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 150..276
id W60505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..346
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 270..311
id W60505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 38..312
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..275
id W60589
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..346
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 269..310
id W60589
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..144
id R33763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 144..229
id R33763
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 268..312
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 238..282
id R33763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..337
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 276..308
id R33763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 3..146
id AA123856
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..346
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 88..253
id HSB31E112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..181
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..89
id HSB31E112
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..375
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq SLVLLTVTPSXRQ/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
AGGACTTCCC CCGGGCTGAG CTGCGCASGG GGTTTTGGCC AAATTGGGCG AGGGCACAAA   60
ATAACCACTT ACCCCTTCTC ACCGAGGAAG AGCGGGAGAA AGGGT ATG GCA CAG TCA   117
                                     Met Ala Gln Ser
                                     -90

DAA GGG TGG GTG RAA AGR TAC KTC AAG GCC TTT TGT AAA GGC TTC TTT   165
Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys Lys Gly Phe Phe
```

-85		-80		-75	
GTG GCG GTG CCT GTG GCA GTG ACT TTC TTG GAT CGG GTC GCC TGT GTG	213				
Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg Val Ala Cys Val					
-70		-65		-60	-55
GCA AGA GTA GAA GGA GCA TCG ATG CAG CCT TCT TTG AAT CCT GGG GGG	261				
Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu Asn Pro Gly Gly					
		-50		-45	-40
AGC NAG TCA TCT GAT GTG GTG SDD DTG AAC CAC TGG AAA GTG AGG AAT	309				
Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp Lys Val Arg Asn					
		-35		-30	-25
TTT GAA GTA CAC CGT GGT GAC ATT GTA TCA TTG GTG TTG CTC ACT GTG	357				
Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val Leu Leu Thr Val					
		-20		-15	-10
ACG CCC TCC ASC CGA CAA CAG GAG	381				
Thr Pro Ser Xaa Arg Gln Gln Glu					
-5		1			

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 11..158
id H56585
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 201..322
id H56585
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 151..322
- (C) IDENTIFICATION METHOD: blastn

- (D) OTHER INFORMATION: identity 93
region 119..290
id AA147898
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 39..159
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..128
id AA147898
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 201..322
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..204
id R52248
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 170..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 51..83
id R52248
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 177..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 87..174
id H54950
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 284..315
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 192..223
id H54950
est
- (ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: complement(199..320)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 40..161
id W22146
est
- (ix) FEATURE:
(A) NAME/KEY: sig_peptide

(B) LOCATION: 67..135
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.1
 seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCCGCTGTT GTTGTGGTCC CCATGGAGCT GCCGTAGCGG ACCCAGCACA GCCAGGAGCG      60
TCCGGG ATG AGC TCA GCC GCG GCC GAC CAC TGG GCG TGG TTG CTG GTG      108
    Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val
          -20                      -15                      -10
CTC AGC TTC GTG TTT GGA TGC AAT GTT CTT AGG ATC CTC CKC CCG GBC      156
Leu Ser Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa
          -5                      1                      5
YTC STM ATC STG CAK GTC CAG GGT GCT GCA GAA GGA CGC GGA SAG GAG      204
Xaa Xaa Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu
          10                      15                      20
TCA CAG ATG AGA GCG GAG ATC CAG GAC ATG AAG CAG GAG CTC TCC ACA      252
Ser Gln Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr
          25                      30                      35
GTC AAC ATG ATG GAC GAG TTT GCC AGA TAT GCC AGG CTG GAN AGA AAG      300
Val Asn Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys
          40                      45                      50                      55
ATC AAC AAG ATG ACG GAT AAG      321
Ile Asn Lys Met Thr Asp Lys
          60
  
```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 196..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 10..196
 id HSC2EA121
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 121..205
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 134..218
 id AA095017
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 197..252
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 209..264
 id AA095017
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 281..340
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8
 seq HVFFLLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

GTTTTTGT2TTT GTGTGTGCGT GTTGTGGGCC TCCATCCCCA CTCCCCAGAC TCCACTTCTC      60
CAGGCCTCTC TCCCGCCTTT TCATCCCGCA TCCGCAGGAC ACCCAATCAC CGGGGCAACA      120
GGATGCCTTC CGCGCCTTCC ACCCTGACCT GGAATTCGTG GGCAAGTTCT TGAAACCCCT      180
GCTGATTGGT GAACTGGCCC CGGAGGAGCC CAGCCAGGAC CACGGCAAGA ACTCAAAGAT      240
CACTGAGGAC TTCCGGGCCC TGAGGAAGAC GGCTGAGGAC ATG AAC CTG TTC AAG      295
                                     Met Asn Leu Phe Lys
                                     -20

ACC AAC CAC GTG TTC TTC CTC CTC CTC CTG GCC CAC ATC ATC GCC CTG      343
Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala His Ile Ile Ala Leu
-15                      -10                      -5                      1

GAG AGC ATT GCA TGG TTC ACT GTC TTT TAC TTT GGC AAT      382
Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe Gly Asn
          5                      10

```

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 101..321
id H21228
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 117..357
id R72127
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..59
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 77..117
id R72127
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..204
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 63..207
id H18908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 195..269
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 199..273
id H18908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..59
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 23..63
id H18908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95

(A) NAME/KEY: other
(B) LOCATION: 19..59
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 98..138
id W93461
est

(A) NAME/KEY: other
(B) LOCATION: 252..288
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 333..369
id W93461
est

(A) NAME/KEY: other
(B) LOCATION: 228..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 308..339
id W93461
est

```
(A) NAME/KEY: other  
(B) LOCATION: 136..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
                        region 93..257  
                        id HUM085F04B  
                        est
```

(A) NAME/KEY: sig_peptide
(B) LOCATION: 170..241
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

AATCACGTGG	CTGCCACCCA	GGGGCATTCT	TCGGGGGTGC	ATCAGAGGGA	GGGCAGAGCC	60
TGAGGATCTA	AGCGAAGGCT	TCCCCGGGTG	TAATTTCTCT	GGCTGTTTGT	GAGGAGAGAT	120
CGAATTCGCC	TCCTGCTCTC	AGGCCTCTCT	GCTCCTGTCT	TTTGTTTGG	ATG CCG GCG	178
					Met Pro Ala	
CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG						226
Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu						
-20		-15		-10		

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT 274
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp
-5 1 5 10
TCC GGC TCT GGC TAC GTT CCG GGC 298
Ser Gly Ser Gly Tyr Val Pro Gly
15

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..286
id HUM085F04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 167..265
id R64509
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 118..180
id R64509
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 245..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 266..307
id R64509
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 182..297
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 133..195
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 159..350
id H21228
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 151..236
id AA009893
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..206
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 97..155
id AA009893
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 49..110
id AA009893
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..198
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```

ATG ATA GGG TCG GGA TTG GCT GGC TCT GGA GGC GCA GGT GGT CCT TCT      48
Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
   -65                      -60                      -55

TCT ACT GTC ACA TGG TGC GCG CTG TTT TCT AAT CAC GTG GCT GCM ACC      96
Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr
-50                      -45                      -40                      -35

CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG CTG CTG CCT     144
Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
                      -30                      -25                      -20

GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC     192
Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala
                      -15                      -10                      -5

TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT TCC GGC TCT     240
Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser
      1                      5                      10

GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT GTT ACT TGC CCC AGG     298
Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg
  15                      20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 53..340
id AA056366
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 80..367
id R77008
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 77..268
id W75983
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 269..365
id W75983
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 129..320
id W39055
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 321..417
id W39055
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 84..288
id N48534
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 318..373
id N48534
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

ATTTGTTTGG ATG CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG	49
Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu	
-20 -15	
CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG	97
Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser Pro Thr Gln	
-10 -5 1 5	
CCC TCG CCG GCC TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC	145
Pro Ser Pro Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val	
10 15 20	
TCT GCA GCC TTT GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC	193
Ser Ala Ala Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile	
25 30 35	
GCC AGG GCC GTG GTG GAG AAG CGC CTA GCA GCC TGC GTC AAC CTC ATC	241
Ala Arg Ala Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile	
40 45 50	
CCT CAG ATT ACA TCC ATC TAT GAG TGG AAA GGG AHG ATC GAG GAA GAC	289
Pro Gln Ile Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp	
55 60 65	
AGT GAG GTG CTG ATG ATG ATT AAA ACC CAA GCG	322
Ser Glu Val Leu Met Met Ile Lys Thr Gln Ala	
70 75 80	

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 247..302
id T80036
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..308

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

AAGATGGAAC TGGTAGTCAG CTGGAGAGCA GC	ATG GAG GCG TCC TGG GGG AGC	53
	Met Glu Ala Ser Trp Gly Ser	
	-90	
TTC AAC GCT GAG CGG GGC TGG TAT GTC TCT GTG CAG CAG CCT GAA GAA	101	
Phe Asn Ala Glu Arg Gly Trp Tyr Val Ser Val Gln Gln Pro Glu Glu		
-85 -80 -75 -70		
GCG GAG GCC GAA GAG TTG AGT CCG TTG CTA AGC AAC GAA CTT CAC AGA	149	
Ala Glu Ala Glu Glu Leu Ser Pro Leu Leu Ser Asn Glu Leu His Arg		
-65 -60 -55		
CAG CGA TCC CCA GGT GTT TCA TTT GGT TTA TCA GTG TTT AAT TTG ATG	197	
Gln Arg Ser Pro Gly Val Ser Phe Gly Leu Ser Val Phe Asn Leu Met		
-50 -45 -40		
AAT GCC ATC ATG GGA AGT GGC ATC CTT GGC TTA GCT TAT GTT ATG GCT	245	
Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Val Met Ala		
-35 -30 -25		
AAT ACC GGT GTC TTT GGA TTT AGC TTC TTG CTG CTG ACA GTT GCT CTC	293	
Asn Thr Gly Val Phe Gly Phe Ser Phe Leu Leu Leu Thr Val Ala Leu		
-20 -15 -10		
CTG GCT TCT TAC TCA GTC CAT CTT CTG CTT AGT ATG TGT ATT CAG ACA	341	
Leu Ala Ser Tyr Ser Val His Leu Leu Leu Ser Met Cys Ile Gln Thr		
-5 1 5 10		
GCT GTA ACA TCT TAT GAA GAT CTT GGA CTC TTT GCA TTT GGA TTA CCT	389	
Ala Val Thr Ser Tyr Glu Asp Leu Gly Leu Phe Ala Phe Gly Leu Pro		
15 20 25		
GGA CTG	395	
Gly Leu		

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..132

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..115
id T10447
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 78..128
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
ATTTTGAAGA AGTTCTCCTT TTTGAGGATG AACTTCATGA TCATGGAGTT TCAAGCCTGA    60
GTGTGAAGAT TAGAGTA ATG CCT TCT AGC TTT TTC CTG CTG TTG CGG TTT    110
          Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe
          -15                               -10

TTC TTG AGA ATT GAC GGG GTG CCG    134
Phe Leu Arg Ile Asp Gly Val Pro
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..276
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..233
id N83601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..276
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 15..240
id N56180
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..216
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 23..170
id R57553
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 46..75
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..30
id R57553
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..142
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 42..126
id R57171
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..56
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..39
id R57171
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 142..182
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 97..137
id N88966
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 49..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..35
id N88966
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

AGTCTTTGTC CTGAGCCCAC GATTCCAGAG CTGGCTGGAC CCAAGGAGGT GAAGAGTCAC   60
TTTTCAGCCC CAGGAAGGGC AAAGAAGAGA GARAATCAGC CTGTCTGCTC TCTCCTTGGC  120
TCAACAAGGC CTCTAACAGT CTTCTGTCCT CTATTCTGCA CACGGCATAT TTGGGAACGA  180
GAAACAAAAG TTTTCCCAA ATG AAG AGA ACT CAC TTG TTT ATT GTG GGG ATT   232
                Met Lys Arg Thr His Leu Phe Ile Val Gly Ile
                        -15                               -10

TAT TTT CTG TCC TCT TGC AGG GCA GAA GAG GGG CTT AAT TTC CCC ACA   280
Tyr Phe Leu Ser Ser Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr
                -5                               1                               5

TAT GAT GGG AAG GAC CGA GTG GTA AGT CTT TCC GAG AAG AAC TTC AAG   328
Tyr Asp Gly Lys Asp Arg Val Ser Leu Ser Glu Lys Asn Phe Lys
                10                               15                               20

CAG GTT TTA   337
Gln Val Leu
25

```

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 57..182
id AA019348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 215..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 173..287
id AA019348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..98

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..56
id AA019348
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..217
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..176
id AA013099
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 211..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 171..289
id AA013099
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..56
id AA013099
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 215..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 130..234
id R54717
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 142..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 58..139
id R54717
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 10..64
id R54717
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 105..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..69
id AA112675
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 215..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 108..160
id AA112675
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 185..218
id AA112675
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 62..91
id AA112675
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 88..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 3..138
id H27167
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 215..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 129..233
id H27167
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 145..213
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq VLLLAALPPVLLP/GA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGAGTGTTCG CCGCCGCCGC GGCCGCCACC TGGAGTTTCT TCAGACTCCA GATTTCCCTG      60
TCAACCACGA GGAGTCCAGA GAGGAAACGC GGAGGAGACA ACAGTACCTG ACGCCTCTTT      120
CAGCCCGGGA TCGCCCCAGC AGGG ATG GGC GAC AAG ATC TGG CTG CCC TTC      171
                               Met Gly Asp Lys Ile Trp Leu Pro Phe
                               -20                               -15

CCC GTG CTC CTT CTG GCC GCT CTG CCT CCG GTG CTG CTG CCT GGG GCG      219
Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro Gly Ala
                               -10                               -5                               1

GCC GGC TTC ACA CCT TCC CTC GAT AGC GAC TTC ACC TTT ACC CTT CCC      267
Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro
                               5                               10                               15

GCC GGC CAG AAG GAG TGC TTC TAC CAG CCC ATG CCC CTG RAG GCC TCG      315
Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Xaa Ala Ser
                               20                               25                               30

CTG GAG ATC GAG      327
Leu Glu Ile Glu
35

```

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..250
id HSU52870
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 156..311
id T35951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 7..107
id T35951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 109..166
id T35951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 156..302
id T35949
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 7..107
id T35949
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 109..166
id T35949
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 233..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 53..229
id W17267
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..476
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 220..295
id W17267

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..399
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 54..271
 id HSC34G011
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 136..192
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 7..63
 id HSC34G011
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 306..416
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.3
 seq LLSACLVTWGLG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AATTCATTTT TCACTCCTCC CTCCTAGGTC ACACTTTTCA GAAAAGAAT CTGCATCCTG   60
GAAACCAGAA GAAAAATATG AGACGGGGAA TCATCGTGTG ATGTGTGTGC TGCCTTTGGC  120
TKWGTGTGTK GAAGTYCKG CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG  180
AGGGGAACCC GCTGTTCAGA GCTGTGACTG CGGCTGCACT CAGAGAAGCT GCCCTTGGCT  240
GCTCGTAGCG CCGGGCCTTC TCTCCTCGTC ATCATCCAGA GCAGCCAGTG TCCGGGAGGC  300
ADVNG ATG CCC CAC TCC AGC CTG CAT CCA TCC ATC CCG TGT CCC AGG GGT  350
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
      -35                      -30                      -25

CAC GGG GCC CAG AAG GCA GCC TTG GTT CTG CTG AGT GCC TGC CTG GTG   398
His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
      -20                      -15                      -10

ACC CTT TGG GGG CTA GGA GAG CCA CCA GAG CAC ACT CTC CGG TAC CTG   446
Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
      -5                      1                      5                      10

GTG CTC CAM CTA GCC TCC CTG CAG CTG GGA   476
Val Leu Xaa Leu Ala Ser Leu Gln Leu Gly
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 32..225
id AA025879
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..154)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 97..250
id N33067
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(144..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 31..108
id N33067
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..251
id AA132495
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..251
id AA063545
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(23..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 47..240
id N99132
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 59..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq HLLLLLLLPAPTLK/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```

ACACTCGGGC CCCACTCAAG GATGTAGGGC CTTTCTGGC CCCTGACCCC TCCCTGGC      58
ATG GGA GCG TGG GGA CGG GGC TGG CCT TGG GAG GAG CGG CAG GGG CAT      106
Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His
          -25                      -20                      -15

CAC CTC CTT CTG CTG CTT CTC CCT GCT CCT ACC CTC AAG GGC CTG GGG      154
His Leu Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly
          -10                      -5                      1

GCT GCC CAG CTG CCT CTA TGC CCT TCT GGG GGT CTC AGC CCA CTG CTG      202
Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu
          5                      10                      15

ACA CTT CTG CAA TCC GGG      220
Thr Leu Leu Gln Ser Gly
20                      25

```

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..429
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..438
id W27019
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(79..429)

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 91..441
 id W26783
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 284..390
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 343..449
 id W85233
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 57..281
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq LLFIIGLIGCCAT/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

ACTCTCGGTG AGCGCRSCCC GCTCTCCGGG CCGGGTCTTC GCGGGCCACC GGCGCC ATG	59
Met	
-75	
GGC CAG TGC GGC ATC ACC TCC TCC AAG ACC GTG CTG GTC TTT CTC AAC	107
Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu Asn	
-70 -65 -60	
CTC ATC TTC TGG GGG GCA GCT GGC ATT TTA TGC TAT GTG GGA GCC TAT	155
Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala Tyr	
-55 -50 -45	
GTC TTC ATC ACT TAT GAT GAC TAT GAC CAC TTC TTT GAA GAT GTG TAC	203
Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val Tyr	
-40 -35 -30	
ACG CTC ATC CCT GCT GTA GTG ATC ATA GCT GTA AGA GCC CTG CTT TTC	251
Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu Phe	
-25 -20 -15	
ATC ATT GGG CTA ATT GGC TGC TGT GCC ACA ATC CGG GAA AGT CGC TGT	299
Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg Cys	
-10 -5 1 5	
GGA CTT GCC ACG TTT GTC ATC ATC CTG CTC TTG GTT TTT GTC ACA GAA	347
Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr Glu	
10 15 20	
GTT GTT GTA GTG GTT TTG GGA TAT GTT TAC AGA GCA AAG GTG GAA AAT	395
Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu Asn	
25 30 35	
GAG GTT GAT CGC AGC ATT CAG AAA GTG TAT AAG	428
Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys	
40 45	

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 106..364
id N39913
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..108
id N39913
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 39..166
id HUM527C01B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 165..280
id HUM527C01B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..38
id HUM527C01B
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 81..275
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

AAGAGGATTT GGC GCCCTCC TCTGTGGATT CTGGCCAGGC CGGGTTCGGC GGTGCTGTG      60
AGAGCGGGCT TCCCAACACC ATG CCG KCC GCC TTC TCT GTC AGC TCT TTC CCC      113
          Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro
          -65                      -60                      -55

GTC AGC ATC CCA GCC GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG      161
Val Ser Ile Pro Ala Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp
          -50                      -45                      -40

CTC ATG GGG CTG GCC ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC      209
Leu Met Gly Leu Ala Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys
          -35                      -30                      -25

TTG TCC TCC CGA AGC TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA      257
Leu Ser Ser Arg Ser Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu
          -20                      -15                      -10

GTC ATC TTA GTC TAC TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG      305
Val Ile Leu Val Tyr Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met
          -5                      1                      5                      10

AAC TGG AGA TTA TTT TCG MAA TAC CAG TAT TTC GAC TCC AGG GGG ATG      353
Asn Trp Arg Leu Phe Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met
          15                      20                      25

TTC ATT TCT ATA GTA TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC      401
Phe Ile Ser Ile Val Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile
          30                      35                      40

ATT GTG GTT ATG TGG GTA TGG AAG      425
Ile Val Val Met Trp Val Trp Lys
          45                      50

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 133..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 11..43
id HUM153A05B
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 136..177
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq LLLSLFFPLRISL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
ATTTTCTCC GGTACAGCCT GGGAACGTAG GTCCGCGCC TGTGATAAGT AAGGTTGGAT    60
TTTCTCTCC CTGAGGTGAA GGATGCCCGG RAGSCCTCGG CAGGACCGCG CGGAAACGGG   120
CCTTCTGCCC AAAAG ATG CTG CTT CTC TCC TTA TTC TTT CCC CTC AGA ATC    171
      Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile
                        -10                      -5

TCG CTG TCT CCT TCC AAC CAC CTG TGG TCG GCA TCC TCC GGG            213
Ser Leu Ser Pro Ser Asn His Leu Trp Ser Ala Ser Ser Gly
      1                      5                      10
```

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..304
id HSC26A021
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..174

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..158
id W07871
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 192..306
id W07871
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 174..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 159..188
id W07871
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 144..280
id T75539
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 64..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 41..149
id T75539
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 175..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 161..305
id H94774
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 10..151
id H94774
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 228..319
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 203..294
 id W89738
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 43..102
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 22..81
 id W89738
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 82..150
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.6
 seq LILVLQLLLRIRR/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ACTCGCACCC GGAACAACAA AGCAAGGAAG ACGGAGTCCG AGCCTCGGGG GCTCCTAGCA    60
ACGGGCCCGGG GCGGGAGTTC C ATG GAG ACT GGG GAG CGC GCC CGT CTC ATC    111
                        Met Glu Thr Gly Glu Arg Ala Arg Leu Ile
                        -20                               -15

CTC ATC CTT GTC CTC CAG CTT CTC CTT CGC ATC CGA CGC AAC CGG CAG    159
Leu Ile Leu Val Leu Gln Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln
-10                               -5                               1

CAG CGC TGC SCC GCG TCC TCA GCC ACC GCT CCC TCT TCC CAC GGA TGT    207
Gln Arg Cys Xaa Ala Ser Ser Ala Thr Ala Pro Ser Ser His Gly Cys
5                               10                               15

GAT CTT CGT GGT GGA AAG CTA AAT TTT AAA ACC ACC CCA ATG GAT GCA    255
Asp Leu Arg Gly Gly Lys Leu Asn Phe Lys Thr Thr Pro Met Asp Ala
20                               25                               30                               35

GAC AGT GAT GTT GCA TTG GAC ATT CTA ATT ACA AAT GTA GTC TGT GTT    303
Asp Ser Asp Val Ala Leu Asp Ile Leu Ile Thr Asn Val Val Cys Val
40                               45                               50

TTT AGA ACA AGA TGT CGG                                          321
Phe Arg Thr Arg Cys Arg
55

```

(2) INFORMATION FOR SEQ ID NO: 263:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 2..88
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 18..104
id R56970
est
- (ix) FEATURE:
- (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 128..250
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.4
seq ILGCSSVCQLCTG/RQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AGGAGTTAAG AAATGTCGTT CTTCAGATTT AAAAAGAAAA CCTTTACTGA ATCAGCTGAG      60
TGTTAATAAT ACGAATTTCC TTKTCNTGCC AATKCDRMYC TGRDDCAGRA RATCSNWGAA    120
CAGGGWT ATG TGT GGA TTW YAG TTT TCT CTG CCT TGC CTA CGA CTG TTT      169
    Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe
        -40                      -35                      -30
CTG GTT GTT ACC TGT TAT CKT TTA TTA TTA CTC CAC AAA GAA ATA CTT      217
Leu Val Val Thr Cys Tyr Xaa Leu Leu Leu His Lys Glu Ile Leu
    -25                      -20                      -15
GGA TGT TCG TCT GTT TGT CAG CTC TGC ACT GGG AGA CAA ATT AAC TGC      265
Gly Cys Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys
    -10                      -5                      1                      5
CGT AAC TTA GGC CTT TCG AGT ATT CTA AGA ATT TTC CTG AAA GTA CAG      313
Arg Asn Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln
        10                      15                      20
TTT TTC TGT ATC
Phe Phe Cys Ile
        25

```

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 176..352
id W42809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 50..165
id W42809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 116..218
id N99674
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 34..105
id N99674
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..285
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 218..260
id N99674
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..32
id N99674
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 78..210
id R20073
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 267..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 206..303
id R20073
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..67
id R20073
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..105
id N99685
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 105..207
id N99685
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 251..281
id N99685
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..134

id AA154228

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..206
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 134..200
id AA154228
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

ATAATAAAA ATG AAC CCC GTT ACA GAG TCA CCA TCA TGT CTC TTC TCA CCA   51
  Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro
                    -70                    -65                    -60

CCC TCT GAA TCT GCA TTA GCC AGT CAA CTA GCC CTT TCA GCG TCA TGT   99
Pro Ser Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys
                    -55                    -50                    -45

GAC CAG CGC GCC CCA TTC AGC TTG GCT GGT GTC GKT TCA MMA KRA CCC   147
Asp Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro
                    -40                    -35                    -30

AGG CTG GCC AGT CGT CAG GTT GCA CCG CCC TTT GGT TCC CGA GCA TGC   195
Arg Leu Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys
                    -25                    -20                    -15

TGT TTT CTC TCA GCC TTC TCT CCA ACC TTA ACC AAA TCG GCA GCA GCC   243
Cys Phe Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala
                    -10                    -5                    1                    5

ACC TCG ACC GCC CAC ACA TTC CTG GCC AAT CAG CTC AGC TGT TTA TTT   291
Thr Ser Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe
                    10                    15                    20

ACC AAA TGT CTT CAC AAC AAC TAC AGC AGC AGC CTT CGG CTA ACA AAA   339
Thr Lys Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys
                    25                    30                    35

AAG CAG GAA AAA TCC ACA ACA CCC CAG   366
Lys Gln Glu Lys Ser Thr Thr Pro Gln
                    40                    45

```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..86
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 8..92
id AA070287
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..80
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..66
id T10748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..88
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 17..83
id N67981
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..85
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 17..81
id AA069568
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 25..87
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

AAGGCGCGCG CGGCCAGCGT GGGG ATG TCT AGG AGC TCG AAG GTG GTG CTG 51
Met Ser Arg Ser Ser Lys Val Val Leu
-20 -15

GGC CTC TCG GTG CTG CTG ACG GCG GCC ACA GTG GCC GGC GTA CAT GTG 99
Gly Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val

-10

-5

1

AAG CAG CAG TGG GAC
Lys Gln Gln Trp Asp
5

114

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 8..204
id H10448
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..193
id AA127134
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..193
id HUML13653
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 9..205
id HSC18H071
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..197

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 13..176
 id AA194682
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 31..108
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq GVGLVTLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GTCAGGTGGT GGAGGAAAAG GCGCTCCGTC ATG GGG ATC CAG ACG AGC CCC GTC	54
Met Gly Ile Gln Thr Ser Pro Val	
-25 -20	
CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT CTG CTC GGC CTG GCT	102
Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala	
-15 -10 -5	
GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG CCT CAG GTC ACT CTC	150
Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu	
1 5 10	
CTG GAC CCC AGT GAA AAG TAC CTG CTA CGA CTG CTA GAC AAG ACG ACC	198
Leu Asp Pro Ser Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr	
15 20 25 30	
CCC GGG	204
Pro Gly	

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 33..227
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..195
 id W00881
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 167..319
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq VLLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

CATTGCTCT TCTCTTAACT CCTACCTGAA AACCCCATTC CTAAATTATT CACTATATTT	60
CAGACTTCTT CACTCTTCTC CMAAAACCTG AATCAGCTTG TGCTGATTTT TTCCTATCTG	120
CTATCCCTAA AAGGACTAGA CCTTCTTTCT ATCCTTACTC CCCTCA ATG TAT CCA	175
Met Tyr Pro	
-50	
TCT TAC CTC TTG ATT KKS CCT CCC ATT CCC TCA CAG TTC CTG AAA CAG	223
Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe Leu Lys Gln	
-45 -40 -35	
TGC SCC CCC CCG ACC CTA AGC GAC CCC TTT CTG CCC CTG GCC TTG AGG	271
Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu Ala Leu Arg	
-30 -25 -20	
TCC CTT GAC GTG CTG CTC CTG TCT TCT GCT CNB YTA GTB VVC NAT TCC	319
Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val Xaa Xaa Ser	
-15 -10 -5	
TCT CCC TTG GAA TTC ATC AGA	340
Ser Pro Leu Glu Phe Ile Arg	
1 5	

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 253..332
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 159..238
 id AA114672
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 195..293
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq ILLXTFQWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AGGGGTACCT GGTGTCATG GCAGGCGGTA TTGACCGAAG AGCTTGRTGA GGAAGAGCAG      60
CTGCTGAGAA GGCATCGCAA AKAGAAGAAG GAGTTGCAAS CCAAAATTCA GGGCATGAAG      120
AATGCTGTTC CCAAGAATGA CAATGAAGAG GDAGGARGCA GCTCACCGR A GATGTGGCCA      180
AGTTGGAAAA AGAW ATG GAA CAG AAA CAY AGA GAS GAA CTG GAG CAA TTG      230
          Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu
                    -30                      -25

AAG CTG RCT ACT AAG GAG AAT AAG ATT CTG TTG CTG YWA ACA TTT CAA      278
Lys Leu Xaa Thr Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln
    -20                      -15                      -10

ACT TGG TGC TTG AGA ATC AGC CAC CTC GGA TAT CAR AAG CAC AWA AGA      326
Thr Trp Cys Leu Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg
    -5                      1                      5                      10

GRC GGG TGC CTG GAT MSA AGG AGC TCT CTG TGT TGT CCT TGG      368
Xaa Gly Cys Leu Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
          15                      20                      25
  
```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 209..251
id AA013573
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..43)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90

region 153..195
id AA014924
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..122
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TLKFLTLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AGACGAAGCT CGATGAAGAT TTAGAGAGTT CCACTGAATC CGATGTGACT CTG ATG      56
                                     Met

ATG ACA GCA CCT GTT CTA GCA GCT CAG ACT CTG AAG TTT TTG ACG TTA      104
Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr Leu
      -20                      -15                      -10

TTG CAG AAA TCA AAC GCA AAA AGG SCC AAC CTT GAC CGA CTT CAT GAT      152
Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His Asp
      -5                      1                      5                      10

GAA CTT TGG TAC AAC GAT CCA GGC CAG ATG AAT GAT GGA CCA CTC TGC      200
Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu Cys
                        15                      20                      25

AAA TGC AGC GCA AAG GCA AGA CGC ACA GGA ATT AGG CAC AGC ATT TAT      248
Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile Tyr
                        30                      35                      40

CCT GGA GAA GAG GCC ATC AAG CCC TGT CGT CCT ATG ACC AAC AAT GCT      296
Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn Ala
      45                      50                      55

GGC AGA CTT TTC CAC TAC CGG ATC ACA GTM TCC CCG CCT ACG AAC TTT      344
Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn Phe
      60                      65                      70

TTA ACT GAC AGG CCA ACT GTT ATA GAA TAC GAT GAT CAC GAG TAT ATC      392
Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr Ile
      75                      80                      85                      90

TTT GAA
Phe Glu      398

```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

AGTGCAGAAG GTTCTGGGAA GTAGGAGACC CCACTGGCTT TGGTCCCCTA AGA ATG	56
	Mat
GAC TCT GCT GCC TGT GCT GCT GCT GCC ACC CCT GTT CCA GCC CTG GCT	104
Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu Ala	
-25 -20 -15	
TTG GCC HTA GCT CCA GAC CTA GCA CAA GCC CCA CTG GCA CTC CCT GGC	152
Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro Gly	
-10 -5 1 5	
CTG TTA AGC CCA TCT TGC CTT CTC TCC TCT GGA CAA GAA GTA AAT GGG	200
Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn Gly	
10 15 20	
AGT GAA AGA GGA ACT TGT CTC TGG AGG CCC TGG CTG TCT TCC ACA AAT	248
Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr Asn	
25 30 35	
GAC TCC CCA AGG CAG ATG AGG AAG CTG GTG GAT TTG GCT GCT GGT GGG	296
Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly Gly	
40 45 50	
GCA ACG GCT GCT GAG GTC ACC AAG GCT GAA TCC ATR NTC CAT CAC CCT	344
Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His Pro	
55 60 65 70	
GTC AGG CTC TTC TGG	359
Val Arg Leu Phe Trp	

75

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 15..317
id T86266
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 64..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGLLGTTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

AAAGAGCTTC AGCCTGAAGA CAAGGGAGCA GTCCCTGAAG ACGCTTCTAC TGAGAGGTCT      60
GCC ATG GCC TCT CTT GGC CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT      108
  Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
                    -20                      -15                      -10

CTG GGG CTT TTG GGS ACA CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA      156
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys
                    -5                      1                      5

ACA AGT TCT TAT GTC GGT GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC      204
Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser
                    10                      15                      20

AAG GGC CTC TGG ATG GAA TGT GCC ACA YAC AGC ACA GGC ATC ACC CAG      252
Lys Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln
                    25                      30                      35

TGT GAC ATC TAT AGC ACC CTT CTG GGC CTG CCC GCT GAC ATC CAG GCT      300
Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala
                    40                      45                      50                      55

GCC CAG GCC ATG ATG GTG ACA TCC AGT GCA ATC TCC TCC CTG GCC TGC      348

```

Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys		
				60					65					70			
ATT	ATC	TCT	GTG	GTG	GGC	ATG	AGA	TGC	ACA	GTC	TTC	TGC	CAG	GAA	TCC	396	
Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser		
			75					80					85				
CGA	GCC	AGG														405	
Arg	Ala	Arg															
		90															

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 15..243
id T86266
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..231
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGLLGLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

AGCTGCTTGT	GGCCACCCAC	AGACACTTGT	AAGGAGGAGA	GAAGTCAGCC	TGGCAGAGAG	60
ACTCTGAAAT	GASSGATTAG	AGGTGTTCAA	GGRAGCAAAG	AGCTTCAGCC	TGAAGACAAG	120
GGAGCAGTCC	CTGAAGACGC	TTCTACTGAG	AGGTCTGCC	ATG GCC TCT CTT GGC		174
				Met Ala Ser Leu Gly		-20
CTC CAA CTT	GTG GGC TAC	ATC CTA GGC	CTT CTG GGG	CTT TTG GGC	ACA	222
Leu Gln Leu	Val Gly Tyr	Ile Leu Gly	Leu Leu Gly	Leu Leu Gly	Thr	
	-15		-10		-5	
CTG GTT GCC	ATG CTG CTC	CCC AGC TGG	AAA ACA AGT	TCT TAT GTC	GGT	270
Leu Val Ala	Met Leu Leu	Pro Ser Trp	Lys Thr Ser	Ser Tyr Val	Gly	

	1	5	10	
GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC AAG GGC CTC TGG ATG GAA				318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu				
15	20	25		
TGT GCC				324
Cys Ala				
30				

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 19..184
id AA132585
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..54
id N57441
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 272..325
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

ACGCAGCCGT CAGCCGAACA ATTGGATGAC GAGGCCAGG AAGCACGCTG AAACCCTGGG	60
CGGGGGCAAG CTGTGCGACC TCTTCTGCGG CCGGCCTGGA CTAGCTTTAT CGTCATCTGG	120
GAAATTGTTA AAAATGCAAA TTCGCAAGTT TGAGAGCCAT GGTTCGAAGA AACTGCATAA	180

```

GCATACGAAA TAAGTTGCAG CCTCCCGWCT TATACCCTGG TACTTCTAGT CTAAACAGG 240
ATTGACTCT ACTAATCCAG CCTTATACAG G.ATG CTG TGT TCT TTG CTC CTT 292
                               Met Leu Cys Ser Leu Leu Leu
                               -15

TGT GAA TGT CTG TTG CTG GTA GCT GGT TAT GCT CAT GAT GAT GAC TGG 340
Cys Glu Cys Leu Leu Leu Val Ala Gly Tyr Ala His Asp Asp Asp Trp
-10 -5 1 5

ATT GAC CCC ACA GAC ATG CTT AAC TAT GAT GCT GCT TCA GGA ACA ATG 388
Ile Asp Pro Thr Asp Met Leu Asn Tyr Asp Ala Ala Ser Gly Thr Met
10 15 20

AGA AAA TCT 397
Arg Lys Ser

```

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..42
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 14..55
id H32593
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 22..87
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LWYVCPSPGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

AGACGCTGCC CTTCCGCAGC G ATG GCA TCC CGG CTC TGT GGA GGG GCC CTC 51
                               Met Ala Ser Arg Leu Cys Gly Gly Ala Leu
                               -20 -15

TGG TAT GTG TGT CCC TGT CCT TCT GGG GCG TGG ATG GTK CCT GGG 96
Trp Tyr Val Cys Pro Cys Pro Ser Gly Ala Trp Met Val Pro Gly
-10 -5 1

```

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 15..250
id H23844
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 8..237
id AA036876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..251
id H22656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..217
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..183
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 183..219
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..211
id AA100765
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 69..152
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACGTGACCGG GGCCTGAAGC CGGAAGCTAC CTATCTGGTA GGGAGCTCCC CCAGCACCGA    60
AGACTGCG ATG ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC    110
      Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp
      -25                               -20                       -15

CAG CTC GGC TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT    158
Gln Leu Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser
      -10                               -5                               1

GGG GAC CTG GAG AAT GAT GAG CAG GCA DCC AGT GCC ATC TCT GAG CTG    206
Gly Asp Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu
      5                               10                               15

GTC AGC ACA GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC    254
Val Ser Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro
      20                               25                               30

AGG
Arg
35

```

257

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..243

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 6..245
 id H64050
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 15..248
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..234
 id R17172
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 14..248
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..235
 id HSC15C081
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 22..248
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..227
 id AA149663
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 43..248
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 29..234
 id HSU46380
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 24..149
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.4
 seq ITGVILLAVGING/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```

AGGTGCAGGG TCTCGGGCTA GTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT   53
                        Met Ala Ser Pro Ser Arg Arg Leu Gln Thr
                        -40                               -35

AAA CCA GTC ATT ACT TGT TTC AAG AGC GTT CTG CTA ATC KAC ACT NTK   101
Lys Pro Val Ile Thr Cys Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa
      -30                               -25                               -20

ATT TKC TGG ATC ACT GGC GTK ATC CTT CTT GCA GTT GGC ATT TGG GGC   149

```

Ile	Xaa	Trp	Ile	Thr	Gly	Val	Ile	Leu	Leu	Ala	Val	Gly	Ile	Trp	Gly		
-15						-10					-5						
AAG	GTG	AGC	CTG	GAG	AAT	TAC	TTT	KCK	CTT	TTA	AAT	GAG	AAG	GCC	ACC	197	
Lys	Val	Ser	Leu	Glu	Asn	Tyr	Phe	Xaa	Leu	Leu	Asn	Glu	Lys	Ala	Thr		
1				5				10						15			
AAT	GTC	CCC	TTC	GKG	CTC	ATT	GCT	ACT	GGT	ACC	GTC	ATK	ATT	CTT	TTG	245	
Asn	Val	Pro	Phe	Xaa	Leu	Ile	Ala	Thr	Gly	Thr	Val	Xaa	Ile	Leu	Leu		
			20				25						30				
GGC	TAC	CGG														254	
Gly	Tyr	Arg															
		35															

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 19..246
id HUMHG1206
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..222
id C15962
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 35..220
id HUM417F07B
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 2..33
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..32
 id HUM417F07B
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 59..228
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 18..187
 id AA139623
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 94..178
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..85
 id N88476
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 177..228
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 82..133
 id N88476
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..108
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq VLLGSGLTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCGCTTGGT GGCTCCGTCT GTCTGTCCGT CCGCCCGCGG GTGCCATC ATG GCG GAC	57
Met Ala Asp	
-20	
GCG GCC AGT CAG GTG CTC CTG GGC TCC GGT CTC ACC ATC CTG TCC CAG	105
Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile Leu Ser Gln	
-15 -10 -5	
CCG CTC ATG TAC GTG AAA GTG CTC ATC CAG GTG GGA TAT GAG CCT CTT	153
Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr Glu Pro Leu	
1 5 10 15	
CCT CCA ACA ATA GGA CGA AAT ATT TTT GGG CGG CAA GTG TGN YAG CTT	201
Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val Xaa Xaa Leu	
20 25 30	
CCT NGT CTC TTT AGT TAT GCT CAG CAC GGG	231

Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
35 40

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..185)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 93..276
id AA136898
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 30..76
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 110..146
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..119
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 69..105
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 1..35

id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 129..164
id N41630
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 63..94
id N41630
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..31
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 7..36
id N41630
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 19..142
id AA043148
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 61..125
id HUM430A04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..119
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..60
id HUM430A04B
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 98..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```
AACCTCTTCC GAGCGGGGTC ACGGCCCGGC CGTCGGTAAC CTGGTTTCCG AGAGTGCCGG      50
GCGGTCGGCG GGTCAAGGCA GCCCGGGGCC TGACGCC ATG TCC CGG AAC CTG CGC      115
                                     Met Ser Arg Asn Leu Arg
                                     -20                               -15
ACC GCG CTC ATT TTC GGC GGC TTC ATC TCC CTG ATC GGC GCC GCC TTC      163
Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile Gly Ala Ala Phe
                                     -10                               -5                               1
TAT CCC ATC TAC TTC CGA CCC CAT GGG                                     190
Tyr Pro Ile Tyr Phe Arg Pro His Gly
                                     5                               10
```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(97..229)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 10..142
id H62783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 54..192
id T71240
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 356..429

id AA075451

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..140

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 288..348
id AA075451
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 135..222

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 350..437
id AA009954
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 105..140

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 319..354
id AA009954
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 148..216

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 384..452
id W15396
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..117

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 315..352
id W15396
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 206..256

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.1
seq LWCFFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ATGAGTGTTC ATGTTTTTCT GCACTAGAAG GCACTATGTT GAACTATTAA ACTTACCAGC 60

ACTTTCTTTT TCCACTCCAT AGTTTCATTG TACTGACAAC CTCAGCTGGC ATCATGGACC 120


```

ATGAAGAAGC AAGACGAAAA CACACAGGRA GGGAAATCC TGGGATTCTT TTTCTAGGGA 180
TGTAATACAT ATATTTACAA ATAAA ATG CCT CAT GGA CTC TGG TGC TTC CAC 232
                               Met Pro His Gly Leu Trp Cys Phe His
                               -15                               -10

TTG GTC GTT TTG AGC CTT TAC AGC AGT GTA GCC ACA GCC CGG 274
Leu Val Val Leu Ser Leu Tyr Ser Ser Val Ala Thr Ala Arg
          -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 104..226
id W94087
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 12..134
id R37206
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 19..141
id N42384
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..92)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 177..267

id H84930
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(81..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 144..187
id H84930
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 148..270
id H82795
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..62
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SLVAVFLSCGLIS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ATAAATTAGC AGTATTAGTT ATG AGT TTG GTT GCA GTG TTC TTA TCT TGT GGG    53
                Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly
                        -10                                -5

CTG ATT TCC AAA AAC CAC ATG CTG CTG AAT TTA CCA GGG ATC CTC ATA    101
Leu Ile Ser Lys Asn His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile
                1                      5                      10

CCT CAC AAT GCA AAC CAC TTA CTG                                125
Pro His Asn Ala Asn His Leu Leu
    15                      20
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other

- (B) LOCATION: 2..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 4..87
id HUML1521
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 85..120
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 86..121
id HUML1521
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 123..182
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 69..119
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(75..148)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 324..397
id AA132959
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 27..98
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq GALAVGAVPVVLS/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```

AAAGTTGNSA CCCGGACGGC CTCACC ATG ATG AAA CGG GCA GCT GCT GCT GCA      53
                Met Met Lys Arg Ala Ala Ala Ala Ala
                        -20

GTG GGA GGA GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC      101
Val Gly Gly Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala
-13                -10                -5                1

```

ATG GGC TTC ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC CAT 149
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala His
 5 10 15

GGG 152
 Gly

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
 region 14..212
 id H14129
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
 seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

ATTGCCTTCA TTGCCGGC ATG GCC GTC ATT GTG GAT AAA CCC TGG TTC TAT 51
 Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr
 -80 -75

GAC ATG AAG AAA GTT TGG GAG GGA TAT CCC ATA CAG AGC ACT ATC CCT 99
 Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro
 -70 -65 -60 -55

TCC CAG TAT TGG TAC TAC ATG ATT GAA CTT TCC TTC TAC TGG TCC CTG 147
 Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu
 -50 -45 -40

CTC TTC AGC ATT GCC TCT GAT GTC AAG CGA AAG GAT TTC AAG GAA CAG 195
 Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln
 -35 -30 -25

ATC ATC CAC CAT GTG GCC ACC ATC ATT CTC ATC AGC TTT TCC TGG TTT 243
 Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe

-20	-15	-10	
GCC AAT TAC ATC CGA GCT GGG ACT CTA ATC ATG GCT CTG CAT GAC TCT			291
Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser			
-5	1	5	10
TCC GAT TAC CTG CTG GAG TCA GCC AAG ATG TTT AAC TAC GCG GGA TGG			339
Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp			
15	20	25	
AAG AAC ACC TGC AAC AAC ATC TTC ACC GTC TTC GCC ATT GTT TTT ATC			387
Lys Asn Thr Cys Asn Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile			
30	35	40	
ATC ACC CGA CTG GTC ATC CTG CCC TTC TGG ATC CTG CAT TGC			429
Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys			
45	50	55	

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 37..147
id T82645
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLFIYIFLTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

ATAGTATCTA TTGAAAAGGA AGCAGTGTGT ATCT ATG ATT ATA TCT CTG TTC ATC	55
Met Ile Ile Ser Leu Phe Ile	
-15	-10
TAT ATA TTT TTG ACA TGT AGC AAC ACC TCT CCA TCT TAT CAA GGA ACT	103
Tyr Ile Phe Leu Thr Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr	
-5	1
	5

CAA CTC GGT CTG GGT CTC CCC AGT GCC CAG TGG TGG CCT TTG ACA GGT	151
Gln Leu Gly Leu Gly Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly	
10 15 20	
AGG AGG ATG CAG TGC TGC AGG CTA TTT TGT TTT TTG TTA CAA AAC TGT	199
Arg Arg Met Gln Cys Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys	
25 30 35	
CTT TTC CCT TTT CCC CTC CAC CTG ATT CAG CAT GAT CCC TGT GAG CTG	247
Leu Phe Pro Phe Pro Leu His Leu Ile Gln His Asp Pro Cys Glu Leu	
40 45 50 55	
GTT CTC ACA ATC TCT GGG ACT	268
Val Leu Thr Ile Ser Gly Thr	
60	

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..248
id HSC2OD111
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..136
id T77096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..147
id N32450
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LQMLLG FVGRSKS/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCAAG ATG GCG GCG GAG CTG GTG GAG GCC AAA AAC ATG GTG ATG AGT      50
      Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser
                -30                      -25                      -20

TTT CGA GTC TCC GAC CTT CAG ATG CTC CTG GGT TTC GTG GGC CGG AGT      98
Phe Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser
      -15                      -10                      -5

AAG AGT GGA CTG AAG CAC GAG CTC GTC ACC AGG GCC CTC CAG CTG GTG      146
Lys Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val
      1                      5                      10

CAG TTT GAC TGT AGC CCT GAG CTG TTC AAG AAG ATC AAG GAG CTG TAC      194
Gln Phe Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr
      15                      20                      25                      30

GAG ACC CGC TAC GCC AAG AAG AAC TCG GAG CCT GCC CCA CAG CCG CAC      242
Glu Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His
      35                      40                      45

CGG CCC CTG GAC CCC CTG ACC GGG      266
Arg Pro Leu Asp Pro Leu Thr Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..96
id R05622
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 24..92
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 2..70
 id H94933
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 64..243
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq VHALCPLSPLVTT/GC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AACTCTCCAA AAAGCAGAGA CAGCAGGAAG AGGGGAGTGG AGGCAGCCCA TTCACCTGGG      60
GAA.ATG ACT GGG TTG TCG ATG GMC GGT GGC GGB AGC CSA AMG GGG GAY      108
  Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp
    -60                -55                -50

GTG GAS CCG TDC TAC TAT GGT AAR CVT GGG CCC CTG CGC RCC CTT CCT      156
Val Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro
  -45                -40                -35                -30

GAG CCC TCA GGA CCC CTT CCA CCA AGC AGC GGC CTC TCC CAG CCC CAG      204
Glu Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln
          -25                -20                -15

GTC CAT GCT CTG TGC CCC TTA TCT CCC CTG GTT ACC ACG GGC TGC TGC      252
Val His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys
          -10                -5                1

GGG CAG GCT GCG
Gly Gln Ala Ala
      5
                                     264
  
```

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (C) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 157..269
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 95..207
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..112
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 275..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 213..257
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..166
id AA044371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 157..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 149..211
id AA044371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(272..319)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 423..470
id N30852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(225..264)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 478..517
id N30852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(320..349)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 394..423
 id N30852
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(238..271)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 481..514
 id AA044232
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 303..349
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 5..51
 id R78468
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 367..459
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq GLLGXGLXXXSLT/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AAAGTCCTAG AGGGGGTCGG GGTMTGGGTG GACAAGCTTT CCTCGTCCTC TCCCNACAGA   60
GCTGACGTGT CCTGGGTTCC ACCGGGAGCG GGCATTTCCTA CCGGACGGGA GGGTTCGGGG   120
TGTCCGGGGC TGGGGAATAC GTARGGGKTG CSGCGCCGGT GTGGGAAGTT GGGGCGTGTG   180
GCTGCAGTCC CGGGAGTTCT TGGAGGGGGT CGGCCACCG AGCTTCCGGA CCGGCTGATC   240
TGGCCGTAGC TTGCCGGAGG GAGGGCGGAG CTGACTCTCC GTCCCTTCTC CCATCCCCTC   300
SAGTGGTGGG TACGGGCACC TCGCTGGCGC TCTCCTCCCT CCTGTCCCTN GNNSNTCTTT   360
GCTGGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC AMC GAG TGG CTC   408
      Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu
      -30                -25                -20

ACC ATC CAG GGC GGC CTG CTT GGW KCG GGT CTC TTS KRG TYC TCG CTC   456
Thr Ile Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu
      -15                -10                -5

ACT GCG GGG   465
Thr Ala Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 63..344
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97
region 56..337
id AA203498
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 7..65
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100
region 1..59
id AA203498
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 344..385
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97
region 338..379
id AA203498
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 63..292
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 44..273
id W87295
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 292..344
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92
region 274..326
id W87295
est
- (ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..65
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 327..368
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..312
id AA248429
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 313..354
id AA248429
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 76..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..269
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 270..311
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 30..201
id AA249697
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 33..65
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..33
 id AA249697
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 257..289
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 222..254
 id AA249697
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 227..256
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 193..222
 id AA249697
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 19..180
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

ATCTGGCTCA GTTCCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC	51
Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg	
-50 -45	
AGG TCT CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA TAT	99
Arg Ser Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr	
-40 -35 -30	
TCG GTG CTT TTA CCT ACC TAC AAC GAG CGC GAG AAC CTG CCG CTC ATC	147
Ser Val Leu Leu Pro Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile	
-25 -20 -15	
GTG TGG CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA	195
Val Trp Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu	
-10 -5 1 5	
ATT ATA ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT	243
Ile Ile Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala	
10 15 20	
GAA CAG TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA	291
Glu Gln Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro	
25 30 35	

CGA GAG AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CDY SRA ATG AAA 339
Arg Glu Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys
40 45 50

CAT GCA CAG GAA ACT ACA TCA TTA TTA TGG ATS CTG ATC TCT CAC 384
His Ala Gln Glu Thr Thr Ser Leu Leu Trp Xaa Leu Ile Ser His
55 60 65

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 13..245
id AA134651
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 244..281
id AA134651
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 95..353
id W26888
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 7..208
id T66207
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 263..325.
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 208..270
 id T66207
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 39..267
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..229
 id W00383
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 35..304
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 13..282
 id HSC36A071
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..266
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq LLDSSLMASGTAS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AAACCGGGKG TAGACGTACC TCACGGAAGC CGGCTTTGGC CCTGCGGCTK YTACCGTCGC      60
CGCGGAGAAA TTGTTGGATC TGGCAGTCTA GGAATGAATC TCCTCTCAGC CTTAAGCTC     120
ACCTGGTCAG AATCCTTGGA TGAGCCTGTG GGACCGTTCC TCCTAGCCCG GTGGTTTGGA     180
ACCA GTGGCT TTGGGACTGT AAGAGG ATG GAC AAA GAT TCT CAG GGG CTG CTA      233
                               Met Asp Lys Asp Ser Gln Gly Leu Leu
                               -20                               -15

GAT TCA TCC CTG ATG GCA TCA GGC ACT GCC AGC CGC TCA GAG GAT GAG      281
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
-10                               -5                               1                               5

GAG TCA CTG GCA GGG CAG AAG CGA GCC TCC TCC CAG GCC CTG GGC ACC      329
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
                               10                               15                               20

GGG
Gly
                                                                 332

```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 38..138
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 161..252
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..131
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 15..44
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 100..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CLAVSWEAAGCHG/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AAAGGAATAC TGACAGATAA GGCCGGAAAC AAAACTGATG GCTTGAAAAA CATT TTTATG      60
GAATGTATTT ACTATCATTT TGTTTACTA TAGAGGTAG ATG GGA CTC TTA ACT      114
                                     Met Gly Leu Leu Thr
                                     -35

TTT GGG TAC ATT GAA AMC AKG CKG AAA ACT GAA CAC AAT CCT GAT CAT      162
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His
-30          -25          -20

```


CAC	TCC	TGC	CTG	GCT	GTC	TCC	TGG	GAG	GCT	GCC	GGG	TGC	CAC	GGA	GCT	210
His	Ser	Cys	Leu	Ala	Val	Ser	Trp	Glu	Ala	Ala	Gly	Cys	His	Gly	Ala	
-15					-10					-5					1	
GGG	ACA	CAG	CAG	AGC	CCG	CTA	GGT	GTT	GCA	GGG	CCC	TGG	AGG	CCA	AGG	258
Gly	Thr	Gln	Gln	Ser	Pro	Leu	Gly	Val	Ala	Gly	Pro	Trp	Arg	Pro	Arg	
			5					10					15			
CCA	CCC	TGT	GTG	GGG	TCC	CTG	TTG	GCA	GCC	AGG	TCC	CTA	CAC	AAA	CAA	306
Pro	Pro	Cys	Val	Gly	Ser	Leu	Leu	Ala	Ala	Arg	Ser	Leu	His	Lys	Gln	
		20					25					30				
GTA	ATC	CTG	TTT	GGC	CTC	CTA	GGT	TTT	GCA	TAT	GAC	CAC	TGG			348
Val	Ile	Leu	Phe	Gly	Leu	Leu	Gly	Phe	Ala	Tyr	Asp	His	Trp			
	35					40					45					

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 73..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 53..188
id T06781
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig peptide

(B) LOCATION: 12..59
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGCGCGGGAA C ATG GGG CTG TAC GCT GCG GTG GCA GGC GTG CTG GCC GGC      50
      Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly
            -15                -10                -5

GTG GAG AGC CGC CAG GGC TCT AAT CAA GGG GCT GGT GTA CTC CAG CAA      98
Val Glu Ser Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln
            1                5                10

CTT CCA GAA CGT GAA RCA GCT GTA CGC GCT GGT GTG CGA AAS GCA GCG     146
Leu Pro Glu Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala
            15                20                25

CTA CTC CGC CGT GCT GGA TRC CGT GAT CTC CAR CGC CGG CCT CCT CAG     194
Leu Leu Arg Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln
            30                35                40                45

TGC GAA GAA GCT
Cys Glu Glu Ala
                                                    206
  
```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 26..219
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 1..194
 id T06781
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 204..234
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 176..206
 id T06781
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 22..74
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 1..53
 id AA101354
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 71..110
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 51..90
 id AA101354
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..203
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

AAAAGGCGCG CGGGAAC ATG GGG CTG TAT GCT GCA GCT GCA GGC GTG TTG	50
Met Gly Leu Tyr Ala Ala Ala Gly Val Leu	
-60 -55	
GCC GGC GTG GAG AGC CGC CAG GGC TCT ATC AAG GGG TTG GTG TAC TCC	98
Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser	
-50 -45 -40	
AGC AAC TTC CAG AAC GTG AAG CAG CTG TAC GCG CTG GTG TGC GAA ACG	146
Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr	
-35 -30 -25 -20	
CAG CGC TAC TCC GCC GTG CTG GAT GCT GTG ATC GCC AGC GCC GGC CTC	194
Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu	
-15 -10 -5	
CTC CGT GCG GAG AAG AAG CTG CGG CCG CAC CTG GCC AAG GTG CTA GTG	242
Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys Val Leu Val	
1 5 10	
TAT GAG TTG TTG TTG GGA AAG GGC TTT CGA GGG GGT GGG GGC CGA TGG	290
Tyr Glu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp	
15 20 25	
ARG GCC CGG	299
Lys Ala Arg	
30	

(2) INFORMATION FOR SEQ ID NO: 292:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 296..458
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..163
 id R50658
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(413..458)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 442..487
 id AA016001
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 5..196
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AGAA ATG GGT GCT CAG CAC ACA GCA CTT CTT CTA AAT ACA GAG GTG AGG	49
Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg	
-60 -55 -50	
TGG CTT TCT CGA GGT AAA GTT CTT GTA AGA CTT TTT GAA CTT CGT CGT	97
Trp Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg	
-45 -40 -35	
GAA CTT TTG GTT TTC ATG GAT TCT GCT TTT CGA CTA TCT GAT TGT TTA	145
Glu Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu	
-30 -25 -20	
ACA AAT TCA TCT TGG CTG CTA AGA CTT GCA TAT CTT GCA GAT ATT TTT	193
Thr Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe	
-15 -10 -5	
ACT AAA TTA AAT GAA GTT AAT TTG TCA ATG CAA GGA AAA AAT GTG ACC	241
Thr Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr	
1 5 10 15	
GTT TTT ACA GTA TTT GAT AAA ATG TCG TCA TTG TTA AGA AAA TTG GAA	299

Val	Phe	Thr	Val	Phe	Asp	Lys	Met	Ser	Ser	Leu	Leu	Arg	Lys	Leu	Glu		
				20					25					30			
TTT	TGG	GCC	TCA	TCT	GTA	GAA	GAA	GAA	AAC	TTT	GAT	TGT	TTT	CCT	ACA	337	
Phe	Trp	Ala	Ser	Ser	Val	Glu	Glu	Glu	Asn	Phe	Asp	Cys	Phe	Pro	Thr		
			35					40					45				
CTC	AGT	GAT	TTT	TTG	ACT	GAA	ATT	AAT	TCT	ACA	GTT	GAT	AAA	GAT	ATT	385	
Leu	Ser	Asp	Phe	Leu	Thr	Glu	Ile	Asn	Ser	Thr	Val	Asp	Lys	Asp	Ile		
			50				55					60					
TGC	AGT	GCC	ATT	GTG	CAG	CAC	CTA	AGG	GGT	TTG	CGC	GCT	ACT	CTG	TTA	433	
Cys	Ser	Ala	Ile	Val	Gln	His	Leu	Arg	Gly	Leu	Arg	Ala	Thr	Leu	Leu		
		65				70					75						
AAA	TAC	TTT	CCT	GTA	ACA	AAT	GAC									457	
Lys	Tyr	Phe	Pro	Val	Thr	Asn	Asp										
		80				85											

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..206
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 6..183
id AA127902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..160
id AA056679
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(99..247)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 302..450
 id W93399
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 90..237
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 11..158
 id R29154
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 117..191
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AATCCGCGGC AGAGCGGCTG CTTGAGATCT GTTCTGGGG CCTCTGGCGG TGGCGGCCTG      60
TGGCGGCCTG GGGCGGCGCG ACGGCTGGTG CGCAGGTACA CTGATGCTGA AGTACT ATG      119
                                     Met
                                     -25

AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT GTT ATG GTC      167
Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met Val
          -20                      -15                      -10

CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC AGC      215
Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser Ser
          -5                      1                      5

CCT GTT TTC CAA ATA CCT AAA AAC GAC AAC ATG      248
Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
    10                      15

```

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 245..374
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 20..149
 id T41381
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 75..227
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```

AAAAATAAAA TGTAGGCAGC AAAAGTGGAA GAGGAGAGGC AGCTGGTGCA CTAATCCAGG      60
TCAGCAATCT GAAG ATG GTC TTA CGG AGC CTA GTA GAG TAC TCC CAG GAT      110
          Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp
          -50                      -45                      -40

GTC CTG GCG CAT CCT GTG TCA GAA GAG CAT CTC CCA GAT GTG AGC CTC      158
Val Leu Ala His Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu
          -35                      -30                      -25

ATT GGA GAG TTC TCA GAC CCG GCA GAG CTC GGC AAG CTG CTT CAG CTG      206
Ile Gly Glu Phe Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu
          -20                      -15                      -10

GTG CTG GGC TGT GCC ATC AGT TGC GAG AAA AAG CAG GAC CAC ATC CAG      254
Val Leu Gly Cys Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln
          -5                      1                      5

AGA ATC ATG ACG CTG GAA GAA TCG GTT CAG CAT GTG GTG ATG GAA GCC      302
Arg Ile Met Thr Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala
          10                      15                      20                      25

ATC CAA GAG CTC ATG ACC AAA GAC ACT CCT GAC TCC CTG TCA CCA GAG      350
Ile Gln Glu Leu Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu
          30                      35                      40

ACG TAT GGC AAC TTT GAC AGC CAG TCC CGC AGT ACT GGG      389
Thr Tyr Gly Asn Phe Asp Ser Gln Ser Arg Ser Thr Gly
          45                      50

```

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 105..270
id AA084830
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 64..93
id AA084830
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 66..231
id W01570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 26..53
id W01570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..111
id H82170
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 7..115
id N71014
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 238..292
id N35296
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 358..396
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MIHGFCCLAPTTS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

ATGGGGGCGG ASTAGCCGGA GCCGCGAGTC CATTTTGGGG CTGTGCTTGG CGCGTACCGT   60
GCGGTCCCCTG TAGTTGGAGG ACGGGCGGTC GCGCSGGCCT TTCCCACTAG CCGGAGGTCTG  120
GAGATAAGTA CCCGCCGCCC GGCTTCTCTC GGGAAAGCGG GGTGGTCCTC GAACCTTCAG  180
CGAGGGTGGG GAGTTGCCCA GTAGCCTCTA GTTCGTTAGT CAAAACGTGA AAAAAAAGA  240
CCTGCTTTGC CVTGGGAAAT AGTAACCCTG CCAAATACAT CAGCTTGTAG GAGACAGAGG  300
ATGTGATGGA GCTGCTTGAA GAAGATCTCA CATGCCCTAT TTGTTGTAGT CTGTTTG   357
ATG ATC CAC GGG TTT TGC CTT GCT CCC ACA ACT TCT GCA AAA AAT GCT   405
Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..63
id C16698
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 25..86
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 9..70
id H48377
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 38..86
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 7..55
id H19182
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 90..140
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

AAGCCTGGGA	CACCGCCGGC	GGGGAGAGAA	GCGGATCCCC	TCCGAGCCCC	GGCCCCAAGT	60
AACGCGCGCCG	CCCCGAGCC	GCCGTGAGT	ATG	CYT	TGT	113
			Met	Xaa	Cys	
					-15	
						-10
CTC	GCC	TGC	GTT	GAA	GCA	161
Leu	Ala	Cys	Val	Glu	Ala	
			-5			
						1
						5
CCC	GGG					167
Pro	Gly					

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 93..226
id W81645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 31..95
id W81645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 62..195
id W06951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 7..64
id W06951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..179
id W38711
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 24..86
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

GCNGTCGGCT CCGCGGCGCC GCC ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC   53
               Met Ala Asp Val Glu Asp Gly Glu Glu Thr
               -20                               -15

TGC GCC CTG GCC TCT CAC TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC   101
Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly
   -10                               -5               1               5

GAC AAG ATG TTC TCC CTC AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC   149
Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser
               10                               15               20

TGG GAC GTG GAG TGC GAT ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG   197
Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met
               25                               30               35

GAT GCC TGT MTT AGA TGT CAA GCG GGG                               224
Asp Ala Cys Xaa Arg Cys Gln Ala Gly
               40                               45
  
```

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 122..188
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 198..264
 id R58050
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(122..188)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 193..259
 id H98670

est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 273..350
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TAGAAAGTAGC	AGGATCGCCT	TAATAATAAT	AATAGTTTTG	TAGCATGAAG	CCTGAGCATT	60
GTCCAAAGTT	TGGAATGTG	AACGCTGATA	GTCACATCTG	TCCATCTTTC	CACATTTCTA	120
GGATGCTGAC	AGACAGCACC	AAGAAGTAAT	TGCAATTTAT	CGGACACACC	TTCTTAGTGC	180
TGCACAGGTA	AAGAACTACT	TCTCCTTTGG	AAAGAATATT	GCTTTAGAGA	TAATAATTTT	240
TATTTTCAAA	TAAATTTATG	TGAAAGTAAT	TG	ATG	TTT	AAA
			Met	Phe	Lys	Val
						Ala
						Ala
						Pro
						-20
						-25
CCT	ATG	CTT	ATT	TAA	KAA	ATA
Pro	Met	Leu	Ile	Xaa	Xaa	Ile
						Ile
						Met
						Phe
						Leu
						Leu
						Ile
						Ile
						Val
						Cys
						-5
						-10
						-15
GGA	TCT	CCC	AGG	CCG		
Gly	Ser	Pro	Arg	Pro		
						356

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 228..322
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..46)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 363..408
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 315..364
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 67..161
id T32629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 154..246
id T32629
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(87..181)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 230..324
id W61289
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(6..93)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 317..404
id W61289
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(87..181)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 232..326
id N53422
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(3..93)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 319..409
id N53422
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..181
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 78..172
id N50275
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..85
id N50275
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 64..126
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXMCLWSLRNLFs/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AGCTATTTGG ATAGTGTAGC TTTAATGTGC TGCACATGAT ACTGGCAGCC CTAGAGTTCA      60
TAG ATG GAC TTT TGG GAC CCA GCA GTT TTT RAA ATG TGT TTA TGG AGT      108
  Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser
      -20                      -15                      -10

TTA AGA AAT TTA TTT TCC AGG TGC AGC CCC TGT CTA ACT GAA ATT TCT      156
Leu Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser
      -5                      1                      5                      10

CTT CAC CTT GTA CAC TTG ACA GCT GAA AAA AAA CAA CAT GGG AGT AAT      204
Leu His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn
      15                      20                      25

AAT GGG TCG GCG
Asn Gly Ser Ala
      30

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..114
id R56502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 162..258
id R56502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 119..162
id R56502

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq SVPLLSLSHSIGI/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```

AGTGACCAAA TGA CTTAACC ACAGATGGAG TGAAGACAGG GGTAAGTGGT TGGTCTGGTC   60
CC CAGTAGAG CAT TGCTCAC TATAAACCAC AAGCTGCTTC TAATTTATTT GAGRTGKTAW  120
TAAYCGTGGG CCTTKATATT CTGGTCTCTC TTGCTGCAA ATG AGT CCG GCA GGC   174
                               Met Ser Pro Ala Gly
                               -30

AAG CAC AAC TCA GAA AGC AAA TTC ACC TTC TTT GTA GCC CTT GAT GGG   222
Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe Val Ala Leu Asp Gly
          -25                      -20                      -15

TCG GTC CCC CTG TTG TCT CTT TCT CAT TCC ATA GGC ATT TCC CCC ACA   270
Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile Gly Ile Ser Pro Thr
          -10                      -5                      1

AGG
Arg
                                                                273

```

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 149..231
id H15081
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 238..308
id H15081
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(2..71)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 234..303
id H16744
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(78..160)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..230
id R61691
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(2..72)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 236..306
id R61691
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(2..85)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 223..306
id H17833
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(109..160)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..199
id H17833
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 23..73
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVCVGLHTEGPWG/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

ATGTGGTGBT TGTGTCTTAA CT ATG CAC TGG GCC CTT GTC TGC GTC GGC TTG 52
Met His Trp Ala Leu Val Cys Val Gly Leu

-15

-10

```

CAT ACA GAG GGC CCC TGG GGT CGG CCC TCC GGC CTG GCC TCA GCC AGT   100
His Thr Glu Gly Pro Trp Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser
      -5                      1                      5

GGG ATG GAC AGG GCC AGG CAG GCC TCT GAA CTT CCA CCT CCT GGG GCC   148
Gly Met Asp Arg Ala Arg Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala
  10                      15                      20                      25

TCC CAG ACC CCC CAG
Ser Gln Thr Pro Gln
              30

```

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 155..325
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..58
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 170..340
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..62

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..55
id H17763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 168..247
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..52
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 183..222
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 268..307
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 111..263
id AA084554
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 136..306
id R52491
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 20..235
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

AGAGCTCGCT GTGGCCCGG ATG TTC GGT GCA GCT GCC AGA TCC GCT GAT CTA      52
                Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu
                  -70                      -65

GTG CTT CTC GAA AAA AAC CTT CAG GCG GCC CAT GGG TAT GCC CAA GAG      100
Val Leu Leu Glu Lys Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu
  -60                      -55                      -50

GAC AGA GAA CGA ATG CAC AGA DRT ATT GTC AGC CTT GSA CAG AAT CTC      148
Asp Arg Glu Arg Met His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu
  -45                      -40                      -35                      -30

CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG CAA TGC TTC CTC      196
Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu
                -25                      -20                      -15

TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG GGA AAA AGA GTT      244
Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val
                -10                      -5                      1

CCA GCG CAC TTT
Pro Ala His Phe
      5

```

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..114
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..81
id AA094982
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..130

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..79
id T68050
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..84
id AA157180
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..81
id AA186993
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 43..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AGCCGGAGCA AAGTTTCACT TATAGAAGGG AGAGGAGCGA AC ATG GCA GCG CGT	54
Met Ala Ala Arg	
-25	
TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC	102
Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile	
-20 -15 -10	
GTT TGC GAC GTT CCC TCA GCC TCT GCC CGG	132
Val Cys Asp Val Pro Ser Ala Ser Ala Arg	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 16..181
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..394
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 260..338
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..322
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 194..265
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 107..293
id AA128556
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 145..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..94
id AA128556
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 104..234
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 153..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98

region 6..91
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 383..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 235..289
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 115..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 65..188
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 201..268
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..115
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..64
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 245..292
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQPSMIQEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
ATCAGACGCC AGTATAAGCC TTTGAGTCTC AATAGACTGC AGTATCTTAT TGATTGGGGT   60
CGTGTTGATC CTAGTCAACC TATTGACTTA ACCCAGCTTG TCAATGGGAG AGGTGTGACC  120
ATCCAGCCAC TTAAAGGGA TTATGGTGTC CAGCTGGTTG AGGAGGGTGC TGACACCTTT  180
ACGGCAAAAG TTAATATTGA AGTACAGTTG GCTTCAGAAC TAGCTATTGC TGCCATTGAA  240
AAAA ATG GTG GTG TTG TTA CTA CAG CCT TCT ATG ATC CAA GAA GTC TGG   289
Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp
      -15                      -10                      -5
```


ACA THG TAT GCA AAC CTG TTC CAT TCT TTC TTC GTG GAC AAC CCA TTC	337
Thr Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe	
1 5 10 15	
CAA AAA GAA TGC TTC CAC CAG AAG AAC TGG TAC CAT ATT ACA CTG ATG	385
Gln Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met	
20 25 30	
CAA AGA ACC GTG GGT ACC TGG CGG ATC CTG CCA AAT TTC CTG AAG CAC	433
Gln Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His	
35 40 45	
GAC	436
Asp	

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..407
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.5
region 1..326
id HSARSE
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..84
id AA160312
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 149..241
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LAVLLSLAPSASS/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AAAAC TCGAA GTTAATCATT CCCAGCTCAA AGCCTTGTGC AAGTGCTCTC TGCCTTCACG      60
CTTGCTTCCT TTGGGAGAGA ACCTTCCTCT TCTTGATCGG GGATTCAGGA AGGAGCCCAG      120
GRGCAGAGGA AGTAGAGAGA GAGRCAAC ATG TTA CAT CTG CAC CMT TCT TGT      172
                               Met Leu His Leu His Xaa Ser Cys
                               -30                               -25

TTG TGT TTC AGG AGC TGG CTG CCA GCG ATG CTC GCT GTA CTG CTA AGT      220
Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu Leu Ser
                               -20                               -15                               -10

TTG GCA CCA TCA GCT TCC AGC GAC ATT TCC GCC TCC CGA CCG AAC ATC      268
Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro Asn Ile
                               -5                               1                               5

CTT CTT CTG ATG GCG GAC GAC CTT GGC ATT GGG GAC ATT GGC TGC TAT      316
Leu Leu Leu Met Ala Asp Leu Gly Ile Gly Asp Ile Gly Cys Tyr
   10                               15                               20                               25

GGC AAC AAC ACC ATG AGG ACT CCG ARN ATT GAC CGC CTT GCA GAG GAC      364
Gly Asn Asn Thr Met Arg Thr Pro Xaa Ile Asp Arg Leu Ala Glu Asp
                               30                               35                               40

GGC GTG AAG CTG ACC CAA CAC ATC TCT GCC GCA TCT TTG TGC      406
Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
                               45                               50                               55

```

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15.8
seq LLLLLLLRHGAQG/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
-20                               -15                               -10                               -5

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
   1                               5

```

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 14
seq LAMLALLSPLSLA/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
-25 -20 -15 -10

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa
-5 1 5

Xaa Pro Glu Tyr Phe Gln Gln Pro
10 15

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.3
 seq HILFLLLEPVAAA/QT
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala  
-15 -10 -5

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr  
                   1                                  5                                  10

Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro  
   15                                  20                                  25                                  30

Leu Leu Ala Gly Leu Val Ala  
                                   35

## (2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -22..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 12.2  
seq LALALGLAQPASA/RR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu  
           -20                                  -15                                  -10

Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu Leu  
   -5                                  1                                  5

## (2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -20..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 11.9

seq LVLEFLLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser
-20 -15 -10 -5

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
 1 5 10

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
 15 20 25

Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu
 30 35 40

Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
45 50

```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3  
seq PLLLSSLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
-15 -10 -5

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
1 5 10 15

Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr
 20 25 30

Arg Leu Asp Arg Val Tyr Pro Ser Arg
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
 -10 -5 1
Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
 5 10 15
Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
 20 25 30
Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
 35 40 45 50
Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
 55 60 65
Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu
 70 75 80
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
 85 90 95
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile
 100 105 110
Pro Ser Thr Leu Ala Pro Thr Arg
 115 120

```

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LPLLCLFLQGATA/VL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg Arg Leu Gln Leu Pro
 -25 -20 -15

Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala Val Leu Phe Ala Val
 -10 -5 1 5

Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala Leu Trp Xaa Arg Lys
 10 15 20

Leu Gly

```

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq ALALLLVLP LLWP/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val
 -35 -30 -25

Leu Ser Pro Pro Cys Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu
 -20 -15 -10

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys
 -5 1 5

Xaa Pro Ser Pro Ala Arg Arg

```

10

15

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq PLLGLLLSLPAGA/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
 -20 -15 -10

Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
 -5 1 5

Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
 10 15 20 25

Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
 30 35 40

Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
 45 50 55

Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
 60 65 70

Thr Phe Val Ser Arg His Lys Lys Phe Asp Gly Arg
 75 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:



- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq LWLSLLVPSC/LCA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```

Met Leu Leu His Trp Val Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu
 -25 -20 -15

Trp Leu Ser Leu Leu Val Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro
 -10 -5 1

Leu Pro Ser Leu Pro Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
 5 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LLLFSLVSPPTC/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

```

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10

Trp Xaa Thr Pro Pro Thr Arg Trp
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq AMWWLLLWGVQLQA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35 -30 -25 -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
 -15 -10 -5

Leu Gln Ala Trp Pro Xaa Pro Gly Leu Arg Pro Leu Gly Pro Arg Ala
 1 5 10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
15 20 25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
30 35 40 45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
 50 55 60

Gly Leu Xaa Xaa Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Val Leu
65 70 75

Trp Ser Ala Arg Leu Pro Ser Gly Gln Ala Pro Trp Ser Glu Gly
80 85 90

```

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq LLAVLLASWRLWA/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
-35 -30 -25

Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
-20 -15 -10

Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
-5 1 5 10

Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
15 20 25

Ser Leu Ser Lys Ser Pro Gly
30

```

## (2) INFORMATION FOR SEQ ID NO: 320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -55..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq SLLLLSTALNILA/CQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln Leu Gln Lys
-55 -50 -45 -40

Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg Asn Ile Leu
-35 -30 -25

Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu Leu Ser

```

-20

-15

-10

Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu Leu Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu  
-15 -10 -5

Ser Cys Val Gln Ala Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LCLVCLLVHTAFR/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gln Leu Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr  
                           -15                          -10                          -5

Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp  
                           1                                          5                                          10

Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro  
           15                                          20                                          25

Glu Arg  
   30

## (2) INFORMATION FOR SEQ ID NO: 323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq ILLCSVAVXLSPS/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Cys Ile His Xaa Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala  
       -30                                          -25                                          -20

Leu Lys Ile Leu Leu Cys Ser Val Ala Val Xaa Leu Ser Pro Ser Glu  
       -15                                          -10                                          -5                                          1

Pro Leu Ala Pro  
                           5

## (2) INFORMATION FOR SEQ ID NO: 324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal



## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLFFHILFHSCFS/HL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His  
-20 -15 -10 -5  
Ser Cys Phe Ser His Leu Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLCALAWQQSLG/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly Val Lys Ile Tyr  
-65 -60 -55  
Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met Met Asn Ser Ile

-50                      -45                      -40  
 Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu Glu Ser Pro Thr  
     -35                      -30                      -25  
 Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala Leu Ala Trp Gln  
     -20                      -15                      -10                      -5  
 Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val Ser Glu Lys Ala  
                             1                      5                      10  
 Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His Ser Lys Asp Phe Thr  
             15                      20                      25  
 Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His Phe Asn Tyr Pro Ser  
     30                      35                      40  
 Thr Pro Arg  
     45

## (2) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq FVRFLGFSCLQS/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser Tyr Ser Leu Leu Phe  
             -25                      -20                      -15  
 Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln Ser Asp Pro Ile Cys  
             -10                      -5                      1  
 Ser Phe Phe Phe Phe  
     5

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids



(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asp Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser  
                  -20                  -15                  -10  
Ser Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn  
                  -5                          1                  5  
Pro Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu  
          10                          15                          20  
Ala Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro  
  25                          30                          35                  40  
Val Gly Ile Asp Ser Gly Ser Leu  
                          45

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.8  
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Gly Ser Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu

-20

-15

-10

Ser Leu Cys Leu Cys Leu Trp Trp Arg Ile Ile  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq VCLLCSGCSCAWS/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Gln Val Ala Thr Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val  
-30 -25 -20

Lys Pro Val Cys Leu Leu Cys Ser Gly Cys Ser Cys Ala Trp Ser Val  
-15 -10 -5 1

Gly Cys Val Xaa Glu Ser Glu Ser Glu  
5 10

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7

seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser  
           -15                                  -10                                  -5

Thr Ser Gln Pro Gln Arg  
                   1

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5  
seq QCLLCIS?PVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln  
           -30                                  -25                                  -20

Leu Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys  
           -15                                  -10                                  -5

Glu Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys  
   1                                  5                                  10                                  15

Glu Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val  
                   20                                  25                                  30

Ser Pro Leu Ala Ala Trp Met Val  
           35                                  40

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly
 -20 -15 -10
Leu Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His
 -5 1 5
Pro Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser
 10 15 20 25
Asp Arg

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Cys Leu Leu Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe
 -15 -10 -5
Ser Phe Ser Gln Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly
 1 5 10
Ser His Pro Glu Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys
 15 20 25

```

Ala Arg Pro Gln Pro Pro Leu Phe His Pro Phe Ile Ser Ser  
 30 35 40

## (2) INFORMATION FOR SEQ ID NO: 336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLVASGXAEVSA/QS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ala Ser Glu Arg Xaa Pro Asn Arg Pro Xaa Cys Leu Leu Val Ala  
 -25 -20 -15 -10  
 Ser Gly Xaa Ala Glu Gly Val Ser Ala Gln Ser Phe Leu Xaa Cys Phe  
 -5 1 5  
 Thr Met Ala Ser Thr Xaa Phe Asn Leu Gln Val Ala Xaa Pro Gly Gly  
 10 15 20  
 Lys Ala Met Glu Phe Val Asp Val Thr Xaa Ser Asn Ala Arg Trp Val  
 25 30 35  
 Gln Asp  
 40

## (2) INFORMATION FOR SEQ ID NO: 337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
 seq LAFQLVFLRATSG/SC
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```

Met Phe Pro Asp Tyr Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln
-25 -20 -15 -10

Leu Val Phe Leu Arg Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg
 -5 1 5

His Leu His Asn Ile Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly
 10 15 20

Ser Cys Ile Gln Lys Gln Pro Gly
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq LLLXLXLLIIALE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Ile | Ser | Leu | Thr | Ser | Ser | Pro | Val | Arg | Leu | Leu | Leu | Xaa |
| -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |     | -10 |
| Leu | Xaa | Leu | Leu | Leu | Ile | Ala | Leu | Glu | Ile | Met | Val | Gly | Gly | His | Ser |
|     |     |     |     | -5  |     |     |     |     | 1   |     |     |     | 5   |     |     |
| Leu | Cys | Phe | Asn | Phe | Thr | Ile | Lys | Ser | Leu | Ser | Arg | Pro | Gly | Gln | Pro |
|     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |
| Trp | Cys | Glu | Ala | His | Val | Phe | Leu | Asn | Lys | Asn | Leu | Phe | Leu | Gln | Tyr |
|     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |
| Asn | Ser | Asp | Asn | Asn | Met | Val | Lys | Pro | Leu | Gly | Leu | Leu | Gly | Lys | Lys |
| 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu  
                                 60                                65                                70  
 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys  
                                 75                                80

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq TFLLLLFYNAGRS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Thr Phe Leu Leu Leu Leu Phe Xaa Asn Ala Gly Arg Ser Leu Arg  
                                 -10                                -5                                1

Met Cys

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq EMFLVLLVTGVHS/NK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met Phe  
 -25 -20 -15

Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr Ala Lys  
 -10 -5 1 5

Lys Ile Lys Arg Pro Gly  
 10

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Ser Ser Pro Leu Leu Val Glu Gln Ser Ser Thr Lys Ser Pro Lys  
 -40 -35 -30 -25

Ser Trp Ser Trp Ser Phe Leu Ala Phe Ser Cys Ile Ser Leu Leu Phe  
 -20 -15 -10

Ile Phe Phe Ser Ile Ala Asn Ser Ser Pro Cys Gly  
 -5 1

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq IPLLLLFFHLSFL/NS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Tyr Leu Phe Cys Leu Phe Ser Val Ser Lys Thr Ile Pro Leu Leu
-25 -20 -15 -10

Leu Leu Phe Phe His Leu Ser Phe Leu Asn Ser Leu
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq CLLILKFLSPAET/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Ile Val Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr
-15 -10 -5

Ser Ile Leu Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val
 1 5 10 15

Pro Leu Glu Val Ser Gln Ile Leu Gln Thr Gln
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq LILCFLFILHTHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25 -20 -15 -10
Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His
 -5 1 5
```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -36..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
Met Phe Phe Ile Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu
-35 -30 -25
Ala Met Lys Pro Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa
-20 -15 -10 -5
Xaa Ser Asn Gln Leu Pro Val Thr Gly
 1 5
```

(2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LWPFLTWINPALS/IC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
-60 -55 -50 -45

Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
 -40 -35 -30

Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
-25 -20 -15

Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
-10 -5 1

Leu Gly Ser Cys Gly Trp Gln
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Leu Gln Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys
 -15 -10 -5

Leu Cys Cys Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln
 1 5 10 15

Gly Gly Ser Gly Cys Pro
 20

```

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -19..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 6.6  
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

Met Met Asp Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly
 -15 -10 -5

Pro His Gln Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn
 1 5 10

Leu Pro Lys Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp
 15 20 25

Lys Ala Glu Gln Glu Arg Val Glu Val Glu
 30 35

```

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq LLPGLPLVRTSFS/HF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Met Pro Pro Cys Leu Leu Pro Gly Leu Pro Leu Val Arg Thr  
                    -15                    -10                    -5

Ser Phe Ser His Phe Phe Ser Leu Ser Gly Gly Thr Thr Thr Ala Arg  
                    1                            5                            10

Gly.

## (2) INFORMATION FOR SEQ ID NO: 350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.5  
seq GLAMLHVTRGVXG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu Ala Met  
-25                    -20                    -15                    -10

Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg Val Arg Val Xaa Xaa  
                    -5                            1                            5

Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala Leu Ser Ser Xaa Ala  
            10                            15                            20

Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp  
            25                            30

## (2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -24..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 6.4  
seq LLILLCSSPPDRV/SY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

```

Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile Leu Leu
 -20 -15 -10

Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val Leu His
 -5 1 5

Ser Leu Leu Gln Leu Pro Ala Gln
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -20..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 6.4  
seq FALLFLFLVPVPG/HG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Arg Ile His Tyr Leu Leu Phe Ala Leu Leu Phe Leu Phe Leu Val
-20 -15 -10 -5

Pro Val Pro Gly His Gly Gly Ile Ile Asn Thr Leu Gln Lys Tyr Xaa

```



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq GLALVAGTPPSRS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

```

Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly Thr Pro Pro Ser
 -15 -10 -5

Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg
 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq PCVSLWAPRXFA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu Met
 -35 -30 -25

Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu Trp
 -20 -15 -10

Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr Leu
 -5 1 5 10

Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys Asp
 15 20 25

Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His Cys
 30 35 40

Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
 45 50

```



(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu Leu Xaa Leu  
-20 -15 -10

Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa Xaa Cys Pro  
-5 1 5

Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr  
10 15

(2) INFORMATION FOR SEO ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: AMINO ACID  
(C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -81..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
                        seq FLSLLXSVSETPG/SL
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ala Gly Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro
-30 -75 -70

Gly Arg Leu Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg
 -65 -60 -55 -50
 Ala Thr Ala Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln
 -45 -40 -35
 Glu Leu Val Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala
 -30 -25 -20
 Thr Ala Asp Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro
 -15 -10 -5
 Gly Ser Leu Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp
 1 5 10 15

Gly Arg

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LWCFSFISFSLSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Trp Xaa Gly Ser Leu Trp Cys Phe His Ser Phe Ile Ser Phe
 -15 -10 -5
 Ser Leu Ser Ser Ser Arg
 1

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FLLTFFSYSLLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
  -35                      -30                      -25

Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
 -20                      -15                      -10                      -5

Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
                      1                      5                      10

Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
  15                      20                      25

Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
  30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq WILAVGLSLPSSS/XI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```

Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val Gly Leu Ser Leu Pro
  -15                      -10                      -5

Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu Tyr Ser
  1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVFS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35 -30 -25 -20

His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
 -15 -10 -5

Val Phe Ser Leu Lys Gln Leu Lys Lys
 1 5

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LFLNLCILAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```

Met Asn Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys
      -20              -15              -10

Ile Leu Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr
      -5              1              5

Val Ser Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile
      10              15              20              25

Ser Ile Val Tyr Thr Leu
              30

```

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAWGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Met Gln Gly Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr
-40              -35              -30              -25

Ile Lys Met Arg Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp
      -20              -15              -10

Gly Leu Leu Asn Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr
      -5              1              5

Gly Lys Leu Ile Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp
      10              15              20

Tyr Xaa Glu Leu Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe
      25              30              35              40

Asp Phe Trp Arg Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val
      45              50              55

Val Ser Pro Gly Arg
      60

```

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq PXXLLILAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Met Asn Gln Thr His Pro Xaa Xaa Leu Leu Ile Leu Ala His Ile
 -15 -10 -5
Thr Gln Ser Cys Pro Trp Ala His Val Gly Ala Ala Pro Ser Ala Leu
 1 5 10
Leu Ile His Arg Trp Glu Leu Arg Gly Cys Ser Tyr Leu Lys Leu Phe
 15 20 25
Leu Val Met Val Leu Ile Phe Glu Met Leu
 30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq GLVLLLSLAEILF/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

```

Met Gly Leu Pro Glu Arg Arg Gly Leu Val Leu Leu Ser Leu Ala
-20          -15          -10          -5

Glu Ile Leu Phe Lys Ile Met Ile Leu Glu Gly Gly Gly Val Met Asn
          1          5          10

Leu Asn Pro Gly Asn Asn Leu Leu His Gln Pro Pro Ala Trp Thr Asp
          15          20          25

Ser Tyr Ser Thr Cys Asn Val Ser Ser Gly Phe Phe Gly Gly Gln Trp
          30          35          40

His Glu Ile His Pro Gln Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp
          45          50          55          60

Leu Gln His Leu Leu Asp Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro
          65          70          75

Phe Gln Glu Phe Asp Ile Asn Gly Glu Xaa Arg
          80          85

```

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```

Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro Leu
          -25          -20          -15

Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro Val
          -10          -5          1

Ala Leu Val
          5

```

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ALLASLGIAFSRS/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg Arg Leu
-85 -80 -75 -70

Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp Xaa Xaa
-65 -60 -55

Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val Tyr Phe
-50 -45 -40

Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu Leu Tyr
-35 -30 -25

His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu Gly Ile
-20 -15 -10

Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
-55                      -50                      -45

Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40                      -35                      -30                      -25

Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
                -20                      -15                      -10

Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
                -5                      1                      5

Arg Arg Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
-35                      -30                      -25

Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
-20                      -15                      -10

Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
-5                      1                      5                      10

Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala Val Leu Trp
15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLLFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn Thr Asp
-25 -20 -15
His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFLLPPXP2/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Glu Leu Lys Gln Leu Gly Pro Arg Ser Phe Phe Phe Phe Leu
-20 -15 -10
Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LILPALFFFPLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr Ser Leu Ile Leu
-25 -20 -15

Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe His Gly Leu Thr
-10 -5 1 5

Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro Thr
10 15

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LLLCMDLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu Leu Cys

-25 -20 -15 -10
Met Asp Leu Pro His Ser Val Leu Ser Asn Trp
 -5 1

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -21..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5
seq EFLFLGFPSNSWP/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Leu Glu Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe Pro
-20 -15 -10
Ser Asn Ser Trp Pro His Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -18..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.5
seq FLITLFCCCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```
Met Phe Phe Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val
      -15                      -10                      -5

Val Gly Phe Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu
      1                      5                      10

Val Thr Trp Ala Arg Ala Gly
  15                      20
```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5

seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Ala Cys Phe Gly Glu Lys Arg His Ala Lys Ser Cys Leu Leu His
-25 -20 -15 -10

Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Val Asp Arg Asp Glu Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro
-25 -20 -15
Leu Ser Leu Ala Leu Gln Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp
-20 -15 -10 -5
Cys Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly
1 5 10
Gly

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala Ser Leu
      -35                      -30                      -25

Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr Ser Cys
      -20                      -15                      -10

Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser Ser Leu
      -5                      1                      5

Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys Thr Phe
      10                      15                      20                      25

Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile Asn Phe
      30                      35                      40

Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu Phe Leu
      45                      50                      55

Ala Val Pro Arg
      60

```

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq SFLCNFLVSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser
-20                      -15                      -10                      -5

Leu Ser Leu Ser Phe Leu His Gly Arg

```

1

5

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -33..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.4
seq LAYFLCCQGVIFG/SL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

```

Met Asp Ala Leu Glu Arg Gly Ser Leu Arg Asn Glu Gln Ala Leu Val
      -30                -25                -20

Ile Tyr Ala Gly Leu Ala Tyr Phe Leu Cys Cys Gln Gly Val Ile Phe
      -15                -10                -5

Gly Ser Leu Pro Ser Asn Ala Gly Ala Gly Pro Leu Gly Trp Ser Ser
      1                5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -39..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5.3
seq SLWFLPLPTHVYT/HT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser Arg Gly Glu Ala Arg
 -35 -30 -25

Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser Leu Trp Phe Leu Pro
 -20 -15 -10

Leu Pro Thr His Val Tyr Thr His Thr His Ala Asn
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SSMLITILSFIFA/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Val Ser Ser Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu
 -15 -10 -5 1

Gly Tyr His Thr Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe
 5 10 15

Phe Leu His
 20

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu Ala Ser Ser Ala
-15 -10 -5

Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His Leu Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
  (A) NAME/KEY: sig_peptide
  (B) LOCATION: -39..-1
  (C) IDENTIFICATION METHOD: Von Heijne matrix
  (D) OTHER INFORMATION: score 5.2
                          seq LILLHHCSIRVFF/FF
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

```
Met Ile Cys Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu
      -35                      -30                      -25

Asn Arg Met Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His
      -20                      -15                      -10

Cys Ser Ile Arg Val Phe Phe Phe Phe
      -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Lys Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser
-50 -45 -40

Phe Ser Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln
-35 -30 -25

Val Pro Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile
-20 -15 -10

His Glu Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu
-5 1 5 10

Gln Leu

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFKPAFA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Xaa Pro
-15 -10 -5

Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LWSSCWLAFLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```

Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg Arg Phe Gln Lys Gly
           -30                -25                -20

Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp Leu Ala Pro Leu Ala
      -15                -10                -5

Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln Arg Xaa Ala Ser Asn
      1                5                10

Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro Ala Pro Xaa Ala Ser
  15                20                25                30

Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro Trp Ala Ala Lys Met
           35                40                45

Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala Gly Gly
      50                55

```

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ser Lys Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe
-20 -15 -10
Tyr Gln Ile Ser Gly Arg Trp
-3 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro Asp Ser Ala Gly
-15 -10 -5 1
Pro Phe Leu Ser Pro Phe Ser
5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```

Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys
      -30                      -25                      -20
Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala
      -15                      -10                      -5
Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg
      1                      5                      10
Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly
      15                      20                      25                      30
Gly Gly Trp Met Gly Met Trp Val
      35

```

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
      -45                      -40                      -35
Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
      -30                      -25                      -20
Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
      -15                      -10                      -5                      1
Thr Ser Leu Thr Ala Ala Thr

```

5

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -36..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys Pro Leu Leu
-35                               -30                     -25

Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr Leu Leu Trp
-20                               -15                     -10                     -5

Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg Ile Val Xaa
                               1                     5                     10

Ser Tyr Ser Ser Gly Tyr
15

```

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -41..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5

seq RLLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly Pro Gly
 -40 -35 -30

Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu Leu Leu
 -25 -20 -15 -10

Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp Val Asn
 -5 1 5

Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala Ser Leu
 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
 -30 -25 -20

Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
 -15 -10 -5

Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
 1 5 10 15

His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
-20 -15 -10
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
-5 1 5 10
Trp

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLT LQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ile Leu Ser Thr Trp Leu Leu Leu Thr Leu Gln Asn Ser Val Phe
-15 -10 -5
Thr Ser Phe Arg Ile Ser Pro Asn Arg Ile Gln Ser Met Leu Pro Pro
1 5 10 15
Met

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -32..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

```

Met Ala Phe His Ser Tyr Trp Gly Lys Ser Leu Gln Ser Phe Lys Thr
   -30                               -25                               -20

Phe Met Arg Val Cys Ile Val Leu Ala Leu Cys His Thr Ser Arg Pro
   -15                               -10                               -5

Met Ser Tyr His Val Pro Leu Ala Ala Gly Ser Pro Leu Met His Trp
  1                               5                               10                               15

Ser Pro Cys Ser Pro Val Pro Phe Ile Gly
      20                               25

```

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -16..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.9
seq RTLLPLVLHSQS/SC
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Lys Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser
 -15 -10 -5
 Ser Cys Val Phe Trp Lys Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg Phe
 -30 -25 -20 -15
 Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser Pro
 -10 -5 1
 His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu Cys
 5 10 15
 Asn Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
 -25 -20 -15
 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
 -10 -5 1 5
 Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys Thr Gly Val
 10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.8
 seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro Leu
 -15 -10 -5 1
 His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser Met
 5 10 15
 Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
 20 25

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```

Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro Leu Cys
   -70                               -65                               -60

Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu Gln Arg
   -55                               -50                               -45

Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala Arg Leu
   -40                               -35                               -30

Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile Arg Ser
  -25                               -20                               -15                               -10

Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr Phe Ser
           -5                               1                               5

Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn Ser Gly
      10                               15                               20

Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys Met Xaa
      25                               30                               35

Val His
   40

```

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser Phe Gln Lys Val
 -10 -5 1
Pro Gly

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Val Phe Asp Thr Leu Lys Ser Arg Ile Val Leu Phe Leu Asn Ser
 -20 -15 -10
Xaa Phe Pro Ile Ile Cys Ser Arg
 -5 1

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -59..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq IFLFSILLMSLR/T/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```
Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu Cys Ser  
-55 -50 -45
```

```
Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu Leu Gly  
-40 -35 -30
```

```
Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys Ile Phe  
-25 -20 -15
```

```
Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys Asn Tyr  
-10 -5 1 5
```

```
Phe Arg Gly Asn Gly  
10
```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -17..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 4.7
                               seq MLFFLGALCRESG/VP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met Asp Asp Leu Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser
      -15                -10                -5

Gly Val Pro Ser Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala
  1              5              10              15

Glu Met Pro Pro Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu
      20              25              30

Pro Lys Pro Ala Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe
      35              40              45

```

Pro Val Gly Val Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly
 50 55 60
 Leu Gly His Ser Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val
 65 70 75
 Ser Pro Gly
 80

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu Pro Thr Leu
 -25 -20 -15 -10
 Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly Met Glu Gly
 -5 1 5
 Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu Pro Gly Asp
 10 15 20
 His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr Arg Glu Gly
 25 30 35
 Ala Leu Thr Pro Pro Pro Gly
 40 45

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq QTFVSFLSLPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met Leu Val Ser Lys Ile Gln Thr Phe Val Ser Phe Leu Ser Ile Pro
      -15                      -10                      -5

Val Leu Gly Leu Val Pro Asp His Ile Leu Gln Leu Ile Thr Glu Lys
      1                      5                      10

Glu Thr
      15

```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu His His
      -30                      -25                      -20

Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln Ala Phe
      -15                      -10                      -5                      1

Arg Tyr Glu Asp Gly Gln Leu
      5

```

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq ILLWEACTGRCQA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

```

Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys Gln
   -15                      -10                      -5

Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu Val
   1                      5                      10                      15

Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp Ala
                20                      25                      30

Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala Gly
   35                      40                      45

Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val Lys
   50                      55                      60

Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
   65                      70                      75

```

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: . score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Thr Gly Tyr Pro Trp Ala Asn Ser Ile Thr Thr Val Leu Cys Ile
-25 -20 -15 -10

Leu Gly Cys His Gly Asn Leu Cys Cys Glu Pro Ala Val Arg Ala Leu
-5 1 5

Gly

(2) INFORMATION FOR SEQ ID NO: 413:

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 amino acids
      (B) TYPE: AMINO ACID
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (D) DEVELOPMENTAL STAGE: Fetal
      (F) TISSUE TYPE: kidney

(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -24..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 4.6
                               seq IFTALFLXLHSPA/IN
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu
-20 -15 -10

Phe Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -20..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile Phe Leu Met Cys Leu
 -20 -15 -10 -5

Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -33..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Phe Gly Ala Gly Asp Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser
 -30 -25 -20

Gly Gly Ala Arg Leu Ala Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa
 -15 -10 -5

Gly His Gly Asn Glu Phe Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys
 1 5 10 15

Lys Gly Gln Gly Thr Ala Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr
 20 25 30

Ala Pro Ala Xaa Met Ser Thr Pro Thr Ile Leu Val Ala Thr Ala Val
 35 40 45

His Ala Tyr Arg Tyr Thr Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu
 50 55 60

Val Leu Gln Phe Trp
65

(2) INFORMATION FOR SEQ ID NO: 416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -28..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg
 -25 -20 -15

Phe Leu Ser Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser
 -10 -5 1

Trp Asp Val Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile
 5 10 15 20

Arg Ala Val Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
 25 30

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
 -15 -10 -5
 Gly Val Ser Asp Ser Ser Lys
 1 5

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
 (ii) MOLECULE TYPE: PROTEIN
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -50...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Glu Ser Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln
 -50 -45 -40 -35
 Asn Gln Leu Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa
 -30 -25 -20
 Xaa Xaa Ile Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr
 -15 -10 -5
 Tyr Ala Ser Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile
 1 5 10
 Thr Glu Trp Leu
 15

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

```
Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly Val Leu Val Gly
-25                -20                -15                -10
Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val Lys Gly Pro
                -5                1                5
```

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe Leu Leu Cys Pro Leu
-20                -15                -10
Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp Cys Cys Leu Ile Glu
-5                1                5                10
Lys Thr His Arg Gly
                15
```

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -19..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4
seq RGLLLGLAVAAAA/VR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Leu Arg Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala
 -15 -10 -5
Ala Ala Ala Val Arg
 1

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4
seq ILLMIVFSIFLLL/CN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ile Leu Leu Met Ile Val Phe Ser Ile Phe Leu Leu Leu Cys Asn
 -10 -5 1
Leu Thr Asp Phe Tyr Leu Phe Arg Ser Asp Gly
 5 10

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -14..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.4
seq SLLFIFRSILISC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Ser Leu Leu Phe Ile Phe Arg Ser Ile Leu Ile Ser Cys Phe Ser
 -10 -5 1

Gly Asp Phe Phe Phe Phe
 5

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -17..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.3
seq SKVLIQLSQAFWA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Pro Leu Ile Ser Lys Val Leu Ile Gln Leu Ser Gln Ala Phe Trp
 -15 -10 -5

Ala Ser Pro Glu Gly Arg Asn Ser Ser Gly Ser Lys Arg Lys Gln Leu
 1 5 10 15
 Val Ala Ala Val Glu Met Arg Tyr Cys Lys Arg Gln Gln Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser Arg Ser Asn Lys
 5 10 15
 Phe Gln Asn Ser Ser Val Glu Asp Asp Asp Val Val Phe Ile Glu
 20 25 30 35
 Pro Val Gln Pro Pro Pro Ser Val Pro Val Val Ala Asp Gln Arg
 40 45 50
 Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa Glu Leu Gln Gly Asn Asp
 55 60 65
 Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu Ala Ser
 70 75

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

```

Met Asp Thr Gly Glu Ser Phe Ser Pro His Thr Ser Cys Arg Gly His
  -30                      -25                      -20

Trp Arg Ile Leu Leu Leu Thr His Val Pro Pro Trp Ile Leu Glu Asn
-15                      -10                      -5                      1

Pro Ser Cys His Thr Arg Pro Ala Val Asp Thr Gly Glu Ser Phe Ser
          5                      10                      15

Pro Gln Arg
      20

```

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

```

Met Pro Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu
  -30                      -25                      -20

Arg Lys Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser
-15                      -10                      -5                      1

```

Ile Phe Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg
 5 10 15
 His Leu His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys
 20 25 30
 Pro Pro Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu
 35 40 45
 Ser Gln Gly Met Thr Glu Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys
 50 55 60 65
 Asp Phe Met Met

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

Ser Ser Arg Val Phe His Cys Ile Thr His Pro Asn Gly Arg Ile His

30

35

40

Arg Trp

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Ser Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly
 -10 -5 1

Ser Ala Gly Arg Cys Ala Gly Asp Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Ser Ile Ser Leu Ser Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn
 -20 -15 -10 -5

Met Ala Gln Ile Gln Gln Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr
 1 5 10

Ala Leu Lys Asp Leu Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys
 15 20 25

Lys Asp Glu Pro Pro Gly
 30

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVFQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Thr Ala Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly
 -30 -25 -20

Ser Val Ser Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val
 -15 -10 -5

Phe Gln Glu Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr
 1 5 10

Trp Pro Pro Arg
 15

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Trp Ser Arg Pro Val Gln Val Leu Gly Leu Leu Ala Thr Cys Gln
-15 -10 -5
His Ala Pro Ser Pro Ser Phe Lys Gly Glu Thr Cys Thr Glu Ile Glu
1 5 10 15
Ser Val Tyr Leu Ala Pro Met
20

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln Ile
-20 -15 -10
Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Pro Phe Phe Ser Asn Gln Pro Thr Gln Val Ser Val Leu Leu Phe
-25                -20                -15                -10

Phe Cys Cys Ser Pro Leu Tyr Ser Pro Leu Phe Leu Leu Xaa Leu Ile
          -5                1                5

Pro His Gln
      10

```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -44..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40                -35                -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25                -20                -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10                -5                1

```

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
 5 10 15 20
 Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
 25 30 35
 Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
 40 45 50
 Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
 55 60 65
 Pro Leu Arg
 70

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPQCQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu Trp Leu
 -40 -35 -30
 Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His Thr Gly
 -25 -20 -15
 Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro Pro Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -35..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
 seq VLCCLLLIATPTFF/LL
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

```

Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys Ile Gln
-35 -30 -25 -20

Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala Thr Pro
 -15 -10 -5

Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (2) LENGTH: 27 amino acids  
(3) TYPE: AMINO ACID  
(4) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
                        seq AGVSTSVAAVA/AV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser Val Ala Ala Ala
-15 -10 -5

Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 441:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Trp Ile Met Ser Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile
-15                -10                -5                1
Ser His Ser Leu Cys Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
      5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr Arg
-20                -15                -10                -5
Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val Gln
      1                5                10
Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu Leu
      15                20                25

```

Pro Ser
30

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -44..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

```

Met Ile Glu Pro Cys Glu Lys Met Lys His Tyr Asp Met Asn Trp Phe
      -40                      -35                      -30

Leu Cys Met Tyr Glu Cys Phe Phe Phe His Leu Leu Glu Thr Glu Phe
      -25                      -20                      -15

Leu Leu Pro Cys Val His Pro Phe Ser Val Ile Ala Val Tyr Val Phe
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -55..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro Gln Gln Pro Leu
 -55 -50 -45 -40

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
 -35 -30 -25

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10

Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser Ala Ala
 -15 -10 -5

Gly Arg Phe Gly
 1

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Arg Lys Ile Ser His Cys Leu His Cys Trp Pro Glu Ser Gly Ala
    -25                      -20                      -15

Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser Gly Arg Leu Ser Ser
    -10                      -5                      1

Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro Gln Asp Ala Phe Thr
    5                      10                      15                      20

Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys Thr Glu Lys Glu Phe
    25                      30                      35

Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala
    40                      45                      50

Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser
    55                      60                      65

Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met Ser Leu Val Lys Lys
    70                      75                      80

Lys Gly Gln
    85

```

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Cys Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser

```

-20

-15

-10

Ile Thr Leu Thr Ser Ser Ser Thr Thr Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr Ile Pro Ala Leu
-15 -10 -5

Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln Asp Leu Arg Gly
1 5 10 15

Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro Ser
20 25

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq LTSAFLWLPRHLI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Thr Val Arg Tyr Gly Lys Phe Leu Ser Leu Leu Lys Asp Gly Ala
      -90                      -85                      -80

Glu Asn Asp Leu Thr Trp Val Leu Lys His Cys Glu Arg Phe Leu Lys
      -75                      -70                      -65

Gln Gln Gln Thr Ser Ile Lys Ser Ser Leu Leu Cys Leu Gln Gly Asn
      -60                      -55                      -50

Tyr Ala Gly His Asp Trp Phe Val Ser Ser Leu Phe Met Ile Met Leu
      -45                      -40                      -35                      -30

Gly Asp Lys Glu Lys Thr Phe Gln Phe Leu His Gln Phe Ser Arg Leu
      -25                      -20                      -15

Leu Thr Ser Ala Phe Leu Trp Leu Pro Arg Leu His Ile Ser Val Arg
      -10                      -5                      1

Leu Gln Ser Val Phe Lys Gly Gly Phe Xaa Ile Leu Arg Thr Leu Tyr
      5                      10                      15

Leu His Ser Xaa Gly Arg
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFVVVLFSGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
      -20                      -15                      -10                      -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu
      1                      5                      10

```

Ala Thr

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -22..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPPWTHA/AI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser
-20 -15 -10

Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu
-5 1 5 10

Met Pro Ser Pro Arg Ile Trp Pro Leu
15

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -40..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEFVIS/RS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Arg Tyr Phe Gln Gly Pro Ser Pro Tyr Ser Glu Ile Glu Ile Glu
 -40 -35 -30 -25
 Leu Cys Asp His Val Tyr Ser Phe Gln Gly Leu Cys Val Asn Leu Leu
 -20 -15 -10
 Leu Gly Phe Glu Pro Val Ile Ser Arg Ser Arg Xaa Ser Ser Leu Ala
 -5 1 5
 Val Glu Ser
 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Xaa Xaa Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu
 -40 -35 -30
 Val Tyr Ala Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu
 -25 -20 -15 -10
 Glu Cys Tyr Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu
 -5 1 5
 Glu Val Ala Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val
 10 15 20
 Leu Val Thr Gly Gly Leu
 25

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```

Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr Arg Asp
   -35                               -30                       -25

Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His Leu Leu
   -20                               -15                       -10

Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
   -5                               1                       5

```

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

```

Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
   -25                               -20                       -15

Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
   -10                               -5                       1                       5

Leu Leu Glu Leu

```

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala Ala Pro
 -15 -10 -5

Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa Leu Xaa
 1 5 10

Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu His Gln
 15 20 25

Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FXLLFXFXFFRQ/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe
-15 -10 -5

Arg Gln Xaa Gly
1

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLFRFSVIMA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
-20 -15 -10

Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala Phe Pro Leu Leu Ser
-15 -10 -5

Ser Lys Val Ser Gln Leu Leu Pro Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Glu Glu Glu Ala Ala Gln Ile Pro Arg Ser Ser Val Trp Glu
-35 -30 -25

Gln Asp Gln Gln Asn Val Val Gln Arg Val Val Ala Leu Pro Leu Val
-20 -15 -10

Arg Ala Thr Cys Thr Ala Val Cys Asp Val Tyr Ser Ala Ala Lys Asp
-5 1 5 10

Arg His Pro Leu Leu Gly Ser Ala Trp
15 20

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
Met Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly Pro
    -70                -65                -60

Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly Ile
    -55                -50                -45

Leu Ser Pro Val Gln Glu Val Arg Ala Ala Glu Glu Gln Ile Lys
    -40                -35                -30                -25

Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu Thr
                -20                -15                -10

Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val Ile
                -5                1                5

Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys Phe
    10                15                20

Arg
    25
```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -117..-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

(2) INFORMATION FOR SEQ ID NO: 465:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met Ile Glu Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp
-10 -5 1

Thr Ile Thr Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu
 5 10 15
 Gln Phe Tyr Leu Pro Ser Phe Leu Leu Leu Glu
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met His Pro Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr
 -75 -70 -65
 Lys His Ser Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His
 -60 -55 -50
 Ile Leu Gly Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr
 -45 -40 -35
 Lys Cys Leu Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile
 -30 -25 -20
 Ala Ile Val Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg
 -15 -10 -5 1
 Arg

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IWPMSASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Ile Trp Pro Met Ser Ala Ser Val Ala Thr Leu Trp Ser Phe Thr
 -10 -5 1
Ser Tyr Ile Ser Tyr Pro Ser Arg Phe Tyr Tyr Asp Ala Trp
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp Phe His Pro
-30 -25 -20
Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu Leu Cys Thr
-15 -10 -5 1
Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn Ala Gln Ile
 5 10 15
Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys Pro Phe Lys
20 25 30
Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu Arg Ile Glu
35 40 45
Cys Gln Gly Asn Gly

50

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Lys Glu Leu Asn Gln Lys Leu Thr Asn Lys Asn Asn Lys Ile Glu
  -85                      -80                      -75

Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys Gln Lys Gln Glu Thr Leu
  -70                      -65                      -60

Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser Val Gln Glu Tyr Glu Glu
-55                      -50                      -45                      -40

Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val Lys Thr Lys Lys Glu Leu
      -35                      -30                      -25

Ala Asp Ser Lys Gln Ala Glu Thr Asp His Leu Ile Leu Gln Ala Ser
      -20                      -15                      -10

Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln Gln Val Glu Val Tyr Lys
      -5                      1                      5

Val Arg Val Leu Leu Phe Lys Ile Lys Lys Met Phe Phe His Val Glu
  10                      15                      20                      25

Val Arg Asn Gly

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
      -110                      -105                      -100

Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
      -95                      -90                      -85

Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
      -80                      -75                      -70

Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
      -65                      -60                      -55                      -50

Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
      -45                      -40                      -35

Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
      -30                      -25                      -20

Leu Glu Lys Asn Arg Leu Leu Leu Cys Ile Leu Ile Ile Val Cys Tyr
      -15                      -10                      -5

Ile Leu Phe Leu Met
      1

```

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSIPSLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Leu Ile Leu Ala Asp Thr Arg Arg Val Gln Gly Gly Thr Leu Gly
 -35 -30 -25

Leu Ile Pro Ala Val Leu Asn Arg Val His Val Ala Tyr Ala Ile Pro
 -20 -15 -10

Ser Ile Pro Ser Leu Phe Cys Gln Arg Trp
 -5 1

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Leu Val Gly Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser
 -20 -15 -10 -5

Asn Thr Ser Ser Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile
 1 5 10

Pro Pro His Gly
 15

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

```

Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
  -40                      -35                      -30

Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
  -25                      -20                      -15

Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
  -10                      -5                      1                      5

Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
      10                      15                      20

Ser Leu Gly
      25

```

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

```

Met Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val
      -15                      -10                      -5

Ser Gly Ile Pro Gly Leu Leu Thr
      1                      5

```


(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val
-45 -40 -35

Gly Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser
-30 -25 -20 -15

Gln Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu
-10 -5 1

Ser Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro
5 10 15

Pro Pro
20

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
-20 -15 -10
Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
-5 1 5 10
Leu Arg Thr Val Lys Met Met Arg Val Met
15 20

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Met Asn Gly Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly
-35 -30 -25 -20
Asp Leu Arg Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu
-15 -10 -5
Leu Leu Gly Ser Xaa Gly
1

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7
seq ILFLLSWGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20                               -15                               -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5                               1                               5                               10

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
15                               20                               25

Ser Arg His Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro
30                               35                               40

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
45                               50                               55

Xaa Thr Ile Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
60                               65                               70                               75

Leu

```

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

```

Met Lys Phe Ile Ser Thr Ser Leu Leu Met Leu Leu Val Ser Ser
-20                               -15                               -10

```

Val His Ser Val Glu Asp Met Asn Phe Arg Val His Leu Gln Tyr Glu
50 55 60 65

Phe Thr Lys Leu Gly Leu Xaa Glu Tyr Leu Xaa Lys Leu Lys His Thr
 70 75 80
 Glu Ser Asp Lys Leu Gln Val Gln Ile
 85 90

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly Leu
 -25 -20 -15
 Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe Arg
 -10 -5 1
 His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe Leu
 5 10 15 20
 Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln
 25 30

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LHLFHELLIRPXQG/WX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

```

Met Gly Ser Gly Tyr Ser His Ser Leu His Leu Phe His Leu Leu Ile
-20                      -15                      -10

Arg Pro Xaa Gln Gly Trp Xaa Xaa Ile Val Pro Ala Cys Phe Trp Arg
-5                      1                      5                      10

Lys Lys Ile Leu Thr Pro Ser Thr Gly Thr Met Glu Leu Leu Gln Val
15                      20                      25

Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser Asn Ser Thr Gly
30                      35                      40

Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr Thr Thr Lys Pro
45                      50                      55

Ser Ile Thr Thr Pro Asn Thr Trp
60                      65

```

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

```

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15                      -10                      -5

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
1                      5                      10                      15

Gln Val Ser Cys Arg Ile Met Xaa Xaa Thr Leu Val Ser Lys Lys Ala
20                      25                      30

```

Asn Gln Gln Leu Asn Phe Thr Glu Xaa Xaa Gly Gly Xaa Xaa Ala Ala
 35 40 45
 Gly Thr Lys Phe Gly
 50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq MTCLSVLFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu
 -30 -25 -20
 Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr
 -15 -10 -5
 Ser His Pro Gln Gly Leu Tyr Ile
 1 5

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```
Met Pro Gln Gln Pro Val Glu Gln Gly Ser Pro Leu Leu Arg Gln Leu  
-25 -20 -15
```

Leu Leu Pro Leu Pro Pro Phe Ser Phe Pro Ala Pro Ser Pro Cys Pro
-10 -5 1 5

Ser Trp Pro Val Ala Leu Gly Ser His Gly Val Ala Tyr Trp Gly Ser
10 15 20

Cys Ser Leu Gly His
25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```
Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala  
-80 -75 -70 -65
```

Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Ser Val Arg
-60 -55 -50

Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser
-45 -40 -35

Ala Arg Arg Trp Pro Arg Arg Asp Ala Asp Thr Trp Cys Ala Pro Gln
-30 -25 -20

Gly Val Met Arg Ala Ser Leu Leu Pro Met Leu Leu Gly Ser Trp Ala
-15 -10 -5

Phe Leu Pro Pro Ser Cys Ser Pro Arg Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LTYGIILTHGASG/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Ser His Thr Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu
-40                -35                -30                -25

Leu Asp Ala Val Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile
                -20                -15                -10

Ile Leu Thr His Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met
                -5                1                5

Ser Leu Ala Ser His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe
10                15                20

Thr Cys Lys Gly Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser
25                30                35                40

Val Leu Asn Tyr Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
                45                50                55

```

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -40..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq LCXEFKSVASCD/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                      -35                      -30                      -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Xaa Glu Phe
                      -20                      -15                      -10

Xaa Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                      -5                      1                      5

Xaa Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
    10                      15                      20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Xaa
    25                      30                      35
  
```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Gly Arg Thr Tyr Ile Val Glu Glu Thr Val Gly Gln Tyr Leu Ser
-35                      -30                      -25

Asn Ile Asn Leu Gln Gly Lys Ala Phe Val Ser Gly Leu Leu Ile Gly
-20                      -15                      -10                      -5

Gln Cys Ser Ser Gln Lys Asp Tyr Val Ile Leu Ala Thr Arg Thr Pro
                      1                      5                      10

Pro Lys Glu Glu Gln Ser Glu Asn Leu
    15                      20
  
```

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                      -15                      -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                      1                      5                      10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                      20                      25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                      35                      40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                      50                      55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                      65                      70                      75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                      85                      90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg
95                      100

```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                      -15                      -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                      1                      5                      10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                      20                      25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                      35                      40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                      50                      55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                      65                      70                      75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                      85                      90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
95                      100                     105

Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser Ser Ile
110                     115                     120

Trp Ile Gln Cys Leu Glu
125

```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLEPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20                               -15                -10

Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5                               1                     5                10

Leu His His Ile
15

```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PLIFSLWCSGVLL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```

Met Phe Asn Ala Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe
-40                               -35                -30

Val Phe Thr Phe Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe
-25                               -20                -15                -10

Ser Leu Trp Cys Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly
-5                               1                     5

Gly Pro Arg Leu Trp Arg Ile His Gly Glu Gln
10                               15

```

(2) INFORMATION FOR SEQ ID NO: 494:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -29..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.4
 seq SLLLVQLLTFCSA/QF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
 -25 -20 -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
 -10 -5 1

Val Leu Gly Pro Leu
 5

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -42..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.2
 seq LLFDLVCFEFCQS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30

Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Arg
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq PMQLLQVLSDVLA/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro
 -40 -35 -30
 Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met
 -25 -20 -15
 Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys
 -10 -5 1 5
 Gln Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg
 10 15 20
 Met Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala
 25 30 35
 Thr Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro
 40 45 50
 Val Ile Tyr Pro Val Leu
 55

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Ala Thr Ser Ser Gln Xaa Arg Gln Leu Leu Ser Asp Tyr Gly Pro
                    -75                      -70                      -65
Pro Ser Leu Gly Tyr Thr Gln Gly Thr Gly Asn Ser Gln Xaa Pro Gln
                    -60                      -55                      -50
Ser Lys Tyr Ala Glu Leu Leu Ala Ile Ile Xaa Glu Leu Gly Lys Glu
                    -45                      -40                      -35
Ile Arg Pro Met Tyr Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys
                    -30                      -25                      -20
Arg Gly Ile Ile His Ala Xaa Gly Leu Val Arg Glu Cys Leu Ala Xaa
-15                      -10                      -5                      1
Thr Glu Arg Met Pro Asp Pro Ser Cys Leu Val Gly Phe
                    5                      10
```

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LNSLSALAEQLAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15                -10                -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1          5          10          15

```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq YTAVSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60                -55                -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45                -40                -35                -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25                -20                -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10                -5                1

Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5          10          15

```

Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Thr Thr Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser
-15 -10 -5

Arg Ser Ser Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.1
seq LTL LLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu
 -25 -20 -15 -10
 Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala
 -5 1 5
 Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val
 10 15 20
 Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe
 25 30 35
 Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr
 40 45 50 55
 Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val
 60 65 70
 Gly Ser Ile Leu Ser Glu Gly Glu
 75

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LWSLALWLPLALS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Gly Thr Glu Met Gly Ala Arg Pro Gly Gly His Pro Xaa Lys
 -30 -25 -20
 Trp Ser Phe Leu Trp Ser Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser
 -15 -10 -5
 Val Ser Leu Phe Leu Gly Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu
 1 5 10 15
 Ser Leu Trp Cys Thr Leu Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys
 20 25 30
 Gly Thr Pro Ser Pro Ala Leu Leu Asn Leu Gly Thr Arg Gly
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -55..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.2
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu Ser Leu Gln Val Leu
-55                               -50                               -45                               -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg
                               -35                               -30                               -25

Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly
                               -20                               -15                               -10

Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Xaa His Lys Tyr Pro
                               -5                               1                               5

Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Xaa Ala Leu Thr
10                               15                               20                               25

Val Ala Val Val Val Thr
                               30

```

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.8
 seq MLLLLLLLGSGQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg
 -35 -30 -25
 Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -41..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.9
 seq ILPFLFPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val Thr Ser Asn Thr
 -40 -35 -30
 Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln Ile Leu Pro Phe
 -25 -20 -15 -10
 Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His Xaa Val Ala Gln
 -5 1 5
 Thr Lys Ser Pro Arg
 10

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.7
seq QLCLLLLPCSLVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Pro Gly Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Pro
-20 -15 -10
Ser Cys Ser Leu Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe
-5 1 5 10
Ser Thr Thr Ser Arg Glu
15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -93..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.6
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Arg His Gly Phe Ile Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser
-90 -85 -80
Xaa Xaa Xaa Xaa Ile Phe Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser
-75 -70 -65
Ser Ala Ala Pro Lys His Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu

-60 -55 -50
 Gln Gly Gln Gln Leu Asn Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser
 -45 -40 -35 -30
 Cys Val Leu Ala Ser Ser Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly
 -25 -20 -15
 Leu Ser Leu Ser Leu Gly Ala Ser Ala Pro Val Gln Cys Gln Gln Asp
 -10 -5 1
 Asn Tyr Thr Phe Cys Xaa Gln Tyr Trp Leu Arg Ala Arg His
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LIIFLSFLPFINS/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val Pro Phe Val Arg Gly
 -40 -35 -30
 Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val Ile Leu Ile Ile Phe
 -25 -20 -15 -10
 Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe Val Tyr Lys Thr Asn
 -5 1 5
 Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe Ser Phe Arg Tyr Pro
 10 15 20
 Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu Val Phe
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -20...-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 9.2
                               seq FPVIALFLSGSLA/LF
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Ser Leu Ser Gln Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser
-20 -15 -10 -5

Gly Ser Leu Ala Leu Phe His His Thr Ser Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
      (A) NAME/KEY: sig_peptide
      (B) LOCATION: -29..-1
      (C) IDENTIFICATION METHOD: Von Heijne matrix
      (D) OTHER INFORMATION:  score 8.9
                               seq ALLIVCDVPSASA/QR
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
-10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

(D) OTHER INFORMATION: score 8.5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

(2) INFORMATION FOR SEQ ID NO: 515:

(A) LENGTH: 92 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -90..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION:   score 8.4
                        seq SLVLLTVTPSXK/QE
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Ala Gln Ser Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys
-90 -85 -30 -75

Lys Gly Phe Phe Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg
-70 -65 -60

Val Ala Cys Val Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu
-55 -50 -45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq HVFFLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Asn Leu Phe Lys Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala
-20 -15 -10 -5

His Ile Ile Ala Leu Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe
1 5 10

Gly Asn

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
-20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
-5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly
10 15

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

```

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-65                               -60                               -55

Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr
-50                               -45                               -40                               -35

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
                               -30                               -25                               -20

Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala
                               -15                               -10                               -5

Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser
      1                               5                               10

Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg
15                               20                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION:.. score 7.9
 seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

```

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
      -20                -15                -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
      -5                1                5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
    10                15                20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
    25                30                35                40

Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile Pro Gln Ile
      45                50                55

Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp Ser Glu Val
      60                65                70

Leu Met Met Ile Lys Thr Gln Ala
    75                80
  
```

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (E) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -92..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Glu Ala Ser Trp Gly Ser Phe Asn Ala Glu Arg Gly Trp Tyr Val
      -90                -85                -80

Ser Val Gln Gln Pro Glu Glu Ala Glu Ala Glu Glu Leu Ser Pro Leu
      -75                -70                -65
  
```

Leu Ser Asn Glu Leu His Arg Gln Arg Ser Pro Gly Val Ser Phe Gly
 -60 -55 -50 -45
 Leu Ser Val Phe Asn Leu Met Asn Ala Ile Met Gly Ser Gly Ile Leu
 -40 -35 -30
 Gly Leu Ala Tyr Val Met Ala Asn Thr Gly Val Phe Gly Phe Ser Phe
 -25 -20 -15
 Leu Leu Leu Thr Val Ala Leu Leu Ala Ser Tyr Ser Val His Leu Leu
 -10 -5 1
 Leu Ser Met Cys Ile Gln Thr Ala Val Thr Ser Tyr Glu Asp Leu Gly
 5 10 15 20
 Leu Phe Ala Phe Gly Leu Pro Gly Leu
 25

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Pro
 1

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```

Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser
      -15                -10                -5

Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp
      1                5                10

Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu
      15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Ala Ala
      -20                -15                -10

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
      -5                1                5

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
      10                15                20                25

Tyr Gln Pro Met Pro Leu Xaa Ala Ser Leu Glu Ile Glu
      30                35

```

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq LLSACLVTWGLG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
-35 -30 -25

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
-20 -15 -10

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
-5 1 5 10

Leu Xaa Leu Ala Ser Leu Gln Leu Gly
15 20

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq HLLLLLLPAPTLK/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

```

Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu
-75 -70 -65 -60

Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
-55 -50 -45

Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val
-40 -35 -30

Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu
-25 -20 -15

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
-10 -5 1 5

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr
10 15 20

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
25 30 35

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys
40 45

```

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFLCLVLVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                               -55                               -50
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
-45                               -40                               -35
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
-30                               -25                               -20
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15                               -10                               -5
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
 1                               5                               10                               15
Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
20                               25                               30
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
35                               40                               45
Val Trp Lys
50

```

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LLLSLFFPLRISL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

```

Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile Ser Leu Ser Pro
      -10                      -5                      1
Ser Asn His Leu Trp Ser Ala Ser Ser Gly
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LILVLQLLLRIRR/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

```

Met Glu Thr Gly Glu Arg Ala Arg Leu Ile Leu Ile Leu Val Leu Gln
      -20                      -15                      -10
Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln Gln Arg Cys Xaa Ala Ser
      -5                      1                      5
Ser Ala Thr Ala Pro Ser Ser His Gly Cys Asp Leu Arg Gly Gly Lys
      10                      15                      20                      25
Leu Asn Phe Lys Thr Thr Pro Met Asp Ala Asp Ser Asp Val Ala Leu
      30                      35                      40
Asp Ile Leu Ile Thr Asn Val Val Cys Val Phe Arg Thr Arg Cys Arg

```

45

50

55

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe Leu Val
-40 -35 -30

Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu Gly Cys
-25 -20 -15 -10

Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys Arg Asn
-5 1 5

Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln Phe Phe
10 15 20

Cys Ile
25

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -73..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.4
 seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro Ser
      -70                      -65                      -60

Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys Asp Gln
      -55                      -50                      -45

Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro Arg Leu
      -40                      -35                      -30

Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys Cys Phe
      -25                      -20                      -15                      -10

Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala Thr Ser
              -5                      1                      5

Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe Thr Lys
      10                      15                      20

Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys Lys Gln
      25                      30                      35

Glu Lys Ser Thr Thr Pro Gln
      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
      -20                      -15                      -10

Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
  
```

-5

1

5

(2) INFORMATION FOR SEQ ID NO: 534:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -26..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Ser Glu Lys Tyr Leu
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Pro Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 535:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -51..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.2
seq VLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Tyr Pro Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe
  -50                      -45                      -40

Leu Lys Gln Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu
-35                      -30                      -25                      -20

Ala Leu Arg Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val
                      -15                      -10                      -5

Xaa Xaa Ser Ser Pro Leu Glu Phe Ile Arg
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq ILLXTFQTWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu Lys Leu Xaa Thr
      -30                      -25                      -20

Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln Thr Trp Cys Leu
      -15                      -10                      -5

Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg Xaa Gly Cys Leu
      1                      5                      10                      15

Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TLKFLTLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr
 -20 -15 -10

Leu Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His
 -5 1 5

Asp Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu
10 15 20 25

Cys Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile
 30 35 40

Tyr Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn
 45 50 55

Ala Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn
60 65 70

Phe Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr
75 80 85

Ile Phe Glu
90

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq ALALAXAPDLAQA/PL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu
  -25                      -20                      -15

Ala Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro
  -10                      -5                      1 5

Gly Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn
                      10                      15                      20

Gly Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr
                      25                      30                      35

Asn Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly
                      40                      45                      50

Gly Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His
  55                      60                      65

Pro Val Arg Leu Phe Trp
  70                      75
  
```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -24..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq ILGLLGLLGTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
  -20                      -15                      -10

Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
  -5                      1                      5

Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
  
```

10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Arg
 90

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGLLGTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala
 25 30

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Val Ala Gly
-15 -10 -5
Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
1 5 10
Asp Ala Ala Ser Gly Thr Met Arg Lys Ser
15 20

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq LWYVCPCPSGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Ser Arg Leu Cys Gly Gly Ala Leu Trp Tyr Val Cys Pro Cys
-20 -15 -10
Pro Ser Gly Ala Trp Met Val Pro Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAVLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
 -25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
 -10 -5 1

Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu Val Ser
 5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Arg
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
  -40                      -35                      -30

Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa Ile Xaa Trp Ile Thr Gly
  -25                      -20                      -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 -10                      -5                      1                      5

Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Xaa Leu
   10                      15                      20

Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu Gly Tyr Arg
   25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq VLLGSGLTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

```

Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
-20                      -15                      -10                      -5

Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
   1                      5                      10

Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
   15                      20                      25

Xaa Xaa Leu Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
   30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met	Ser	Arg	Asn	Leu	Arg	Thr	Ala	Leu	Ile	Phe	Gly	Gly	Phe	Ile	Ser
-20					-15					-10					-5
Leu	Ile	Gly	Ala	Ala	Phe	Tyr	Pro	Ile	Tyr	Phe	Arg	Pro	His	Gly	
			1					5					10		

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met	Pro	His	Gly	Leu	Trp	Cys	Phe	His	Leu	Val	Val	Leu	Ser	Leu	Tyr
		-15					-10						-5		
Ser	Ser	Val	Ala	Thr	Ala	Arg									
	1				5										

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SLVAVFLSCGLIS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

```

Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly Leu Ile Ser Lys Asn
          -10                      -5                      1
His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile Pro His Asn Ala Asn
          5                      10                      15
His Leu Leu
          20

```

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq GALAVGAVPVVLS/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

```

Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
          -20                      -15                      -10
Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
          -5                      1                      5

```

Ile Ala Ala Ser Ser Ile Ala Ala His Gly
 10 15

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -91..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met	Ala	Val	Ile	Val	Asp	Lys	Pro	Trp	Phe	Tyr	Asp	Met	Lys	Lys	Val	-30	-75	-70	
Trp	Glu	Gly	Tyr	Pro	Ile	Gln	Ser	Thr	Ile	Pro	Ser	Gln	Tyr	Trp	Tyr	-65	-60	-55	-30
Tyr	Met	Ile	Glu	Leu	Ser	Phe	Tyr	Trp	Ser	Leu	Leu	Phe	Ser	Ile	Ala	-45	-40	-35	
Ser	Asp	Val	Lys	Arg	Lys	Asp	Phe	Lys	Glu	Gln	Ile	Ile	His	His	Val	-30	-25	-20	
Ala	Thr	Ile	Ile	Leu	Ile	Ser	Phe	Ser	Trp	Phe	Ala	Asn	Tyr	Ile	Arg	-15	-10	-5	
Ala	Gly	Thr	Leu	Ile	Met	Ala	Leu	His	Asp	Ser	Ser	Asp	Tyr	Leu	Leu	1	5	10	15
Glu	Ser	Ala	Lys	Met	Phe	Asn	Tyr	Ala	Gly	Trp	Lys	Asn	Thr	Cys	Asn	20	25	30	
Asn	Ile	Phe	Thr	Val	Phe	Ala	Ile	Val	Phe	Ile	Ile	Thr	Arg	Leu	Val	35	40	45	
Ile	Leu	Pro	Phe	Trp	Ile	Leu	His	Cys								50	55		

(2) INFORMATION FOR SEQ ID NO: 551:

(21) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

```

Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
  -30                -25                -20

Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
  -15                -10                -5

Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
  1                    5                10                15

Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
          20                25                30

Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
      35                40                45

Leu Asp Pro Leu Thr Gly
    50

```

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq VHALCPLSPLVTT/GC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```

Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp Val
-60                -55                -50                -45

Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro Glu
          -40                -35                -30

Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln Val
          -25                -20                -15

His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys Gly
      -10                -5                1

Gln Ala Ala
    1

```

(2) INFORMATION FOR SEQ ID NO: 554:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -31..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6
seq GLLGXGLXXXSLT/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

```

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu Thr Ile
  -30                -25                -20

Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu Thr Ala
-15                -10                -5                1

Gly

```

(2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -54..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSES/GI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

```

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu

```

```

-50              -45              -40
Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro
-35              -30              -25
Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val
-20              -15              -10
Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
-5              1              5              10
Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
15              20              25
Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
30              35              40
Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys His Ala Gln Glu Thr
45              50              55
Thr Ser Leu Leu Trp Xaa Leu Ile Ser His
60              65

```

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LLDSSLMASGTAS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

```

Met Asp Lys Asp Ser Gln Gly Leu Leu Asp Ser Ser Leu Met Ala Ser
-20              -15              -10              -5
Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys
1              5              10
Arg Ala Ser Ser Gln Ala Leu Gly Thr Gly
15              20

```

(2) INFORMATION FOR SEQ ID NO: 557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq CLAVSWEAAGCHG/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu
-35 -30 -25

His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala
-20 -15 -10 -5

Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly
1 5 10

Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg
15 20 25

Ser Leu His Lys Gln Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr
30 35 40

Asp His Trp
45

(2) INFORMATION FOR SEQ ID NO: 558:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

```

Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly Val Glu Ser
-15                      -10                      -5

Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln Leu Pro Glu
 1                      5                      10                      15

Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala Leu Leu Arg
      20                      25                      30

Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln Cys Glu Glu
      35                      40                      45

Ala

```

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

```

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
-60                      -55                      -50

Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
-45                      -40                      -35

Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
-30                      -25                      -20                      -15

Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
      -10                      -5                      1

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
      5                      10                      15

Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Arg
      20                      25                      30

```


(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg Trp
      -60                      -55                      -50

Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg Glu
      -45                      -40                      -35

Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu Thr
      -30                      -25                      -20

Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe Thr
      -15                      -10                      -5

Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr Val
  1          5          10          15

Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu Phe
      20          25          30

Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr Leu
      35          40          45

Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile Cys
      50          55          60

Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu Lys
      65          70          75          80

Tyr Phe Pro Val Thr Asn Asp
      85

```

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

```

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25                      -20                      -15                      -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5                      1                      5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

```

Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp Val Leu Ala His
-50                      -45                      -40

Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu Ile Gly Glu Phe
-35                      -30                      -25                      -20

Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu Val Leu Gly Cys

```

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 amino acids
      (B) TYPE: AMINO ACID
      (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo Sapiens
      (D) DEVELOPMENTAL STAGE: Fetal
      (F) TISSUE TYPE: kidney

(ix) FEATURE:
      (A) NAME/KEY: sig peptide
```

(B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 3.7
 seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Xaa Cys Pro Arg Thr Trp Cys Leu Ala Cys Val Glu Ala Ser Pro
 -15 -10 -5

Gly Gln Pro Phe Leu Pro Pro Arg Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 -20 -15 -10

Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 -5 1 5 10

Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 15 20 25

Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Xaa Arg Cys
 30 35 40

Gln Ala Gly
 45

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Phe Lys Val Ala Ala Pro Pro Met Leu Ile Xaa Xaa Ile Ile Met .
-25 -20 -15

Phe Leu Leu Ile Ile Val Cys Gly Ser Pro Arg Pro
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser Leu
-20 -15 -10

Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser Leu
-5 1 5 10

His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn Asn
15 20 25

Gly Ser Ala
30

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq SVPLLSLSHSIGI/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Ser Pro Ala Gly Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe
 -30 -25 -20
Val Ala Leu Asp Gly Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile
 -15 -10 -5
Gly Ile Ser Pro Thr Arg
 1

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LVCVGLHTEGPWG/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met His Trp Ala Leu Val Cys Val Gly Leu His Thr Glu Gly Pro Trp
 -15 -10 -5

Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser Gly Met Asp Arg Ala Arg
 1 5 10 15

Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala Ser Gln Thr Pro Gln
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WFIYIGSSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu Val Leu Leu Glu Lys
 -70 -65 -60

Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu Asp Arg Glu Arg Met
 -55 -50 -45

His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu Leu Asn Phe Met Ile
 -40 -35 -30 -25

Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp Phe Tyr Ile Gly
 -20 -15 -10

Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro Ala His Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart .

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Arg
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQPSMIQEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp Thr
-15 -10 -5

Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe Gln
1 5 10 15

Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met Gln
20 25 30

Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LAVLLSLAPSASS/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Leu His Leu His Xaa Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
-30 -25 -20

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
-15 -10 -5 1

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Met Ala Asp Asp Leu
5 10 15

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro
20 25 30

Xaa Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile
35 40 45

Ser Ala Ala Ser Leu Cys
50 55